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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 : Search time 8.55049 Seconds
(without alignments)
357.079 Million cell updates/sec

Title: US-10-018-924-2_COPY_22_146

Perfect score: 655

Sequence: 1 ARLDVASEFRKKNNKALSR.....FTDKDKNVAPRSKISPOGT 125

Scoring table: BLOSUM62

Searched: Gapex 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	185	1	US-08-233-389C-1
2	655	100.0	185	2	US-08-801-863-1
3	655	100.0	185	2	US-08-486-596A-1
4	655	100.0	185	2	US-09-004-713-1
5	611	93.3	188	1	US-08-233-389C-3
6	611	93.3	188	2	US-08-801-863-3
7	611	93.3	188	2	US-08-486-596A-3
8	611	93.3	188	2	US-09-004-713-3
9	283	42.2	52	4	US-09-070-504-14
10	231	35.3	50	4	US-09-070-504-15
11	163	24.9	31	4	US-09-070-504-23
12	163	24.9	31	4	US-09-011-922A-3
13	163	24.9	31	4	US-09-011-922A-14
14	107	16.3	20	4	US-08-468-249A-20
15	75	11.5	591	2	US-08-966-388A-4
16	67.5	10.3	775	3	US-09-188-403-4
17	67.5	10.3	775	4	US-09-188-404-4
18	67.5	10.3	775	4	US-09-281-259-4
19	65.5	10.0	400	2	US-08-713-388B-2
20	65.5	10.0	400	2	US-08-870-180B-2
21	65.5	10.0	400	3	US-08-814-052-4
22	65.5	10.0	400	3	US-08-812-829-4
23	65.5	10.0	400	3	US-09-226-529-2
24	65.5	10.0	400	3	US-08-870-180B-13
25	65.5	10.0	462	4	US-09-226-529-13
26	65.5	10.0	462	4	US-08-870-180B-13
27	65.5	10.0	467	2	US-08-727-548-2

28	65.5	10.0	467	4	US-08-945-574-1	Sequence 1, Appl1
29	65.5	10.0	754	2	US-08-941-262-1	Sequence 1, Appl1
30	65.5	10.0	755	2	US-08-941-262-3	Sequence 3, Appl1
31	65	9.9	485	1	US-08-453-956-15	Sequence 15, Appl1
32	65	9.9	485	1	US-08-453-956-15	Sequence 15, Appl1
33	65	9.9	485	2	US-08-452-930-15	Sequence 15, Appl1
34	65	9.9	485	2	US-08-452-930-15	Sequence 15, Appl1
35	65	9.9	485	5	PCT-US93-08174-15	Sequence 15, Appl1
36	64.5	9.8	2482	1	US-08-328-254-6	Sequence 15, Appl1
37	63.5	9.7	491	1	US-08-206-176-4	Sequence 4, Appl1
38	63.5	9.7	477	1	US-08-453-956-25	Sequence 25, Appl1
39	63.5	9.7	477	1	US-08-086-631-25	Sequence 25, Appl1
40	63.5	9.7	477	5	US-08-452-930-25	Sequence 25, Appl1
41	62.5	9.5	268	2	US-08-824-874-1	Sequence 25, Appl1
42	62.5	9.5	268	4	US-09-210-084-1	Sequence 1, Appl1
43	62	9.5	410	2	US-08-723-415B-10	Sequence 1, Appl1
44	62	9.5	410	4	US-09-189-627A-10	Sequence 10, Appl1
45	61.5	9.4	454	3	US-08-434-099A-27	Sequence 27, Appl1

ALIGNMENTS

RESULT 1
US-08-233-389C-1
Sequence 1, Application US/08233389C

Patent No. 5639855

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: C/O FISH & MEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,389C

FILING DATE: 26-APR-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-233-389C-1

Query Match

Best Local Similarity 100.0%; Score 655; DB 1; Length 185;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ARLDVASEFRKKNNKALSRKRELRMSSSYPTGLDVAKGAPQTLIRPQDKKASRSE 60

22 ARLDVASEFRKKNNKALSRKRELRMSSSYPTGLDVAKGAPQTLIRPQDKKASRSE 81

QY 61 DSSPDARIRVKRYROSNNFQGLRSGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
DB 82 DSSPDARIRVKRYROSNNFQGLRSGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141

QY 121 SPOGY 125
DB 142 SPOGY 146

RESULT 2
US-08-801-863-1
Sequence 1, Application US/08801863
Patent No. 5830703

GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-801-863-1

Query Match 100.0%; Score 655; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-72;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKMKWMLSRGKRELRMSSYPPTGLADVKGAPQTLIRPDMKGASRSP 60
DB 22 ARLDVASEFRKKMKWMLSRGKRELRMSSYPPTGLADVKGAPQTLIRPDMKGASRSP 81
QY 61 DSSPDARIRVKRYROSNNFQGLRSGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
DB 82 DSSPDARIRVKRYROSNNFQGLRSGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPOGY 125
DB 142 SPOGY 146

RESULT 3
US-08-486-596A-1
Sequence 1, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-596A-1

Query Match 100.0%; Score 655; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-72;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKMKWMLSRGKRELRMSSYPPTGLADVKGAPQTLIRPDMKGASRSP 60
DB 22 ARLDVASEFRKKMKWMLSRGKRELRMSSYPPTGLADVKGAPQTLIRPDMKGASRSP 81
QY 61 DSSPDARIRVKRYROSNNFQGLRSGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
DB 82 DSSPDARIRVKRYROSNNFQGLRSGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPOGY 125
DB 142 SPOGY 146

RESULT 4
US-09-004-713-1
Sequence 1, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JR., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-004-713-1

Query Match 100.0%; Score 655; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-72;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKWKNKALSRGKRELRMSSSYPTGLADVAKGAPQTLIRPQDMKGASRSPE 60
DB 22 ARLDVASEFRKKWKNKALSRGKRELRMSSSYPTGLADVAKGAPQTLIRPQDMKGASRSPE 81
QY 61 DSSPDARIRKRYROSMMNFGILRSFGCGRFGCTGYOKLAHQIYQFTDKDKDNVAPRSKI 120
DB 82 DSSPDARIRKRYROSMMNFGILRSFGCGRFGCTGYOKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPQGY 125
DB 142 SPQGY 146

RESULT 5
US-08-233-389C-3
Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JR., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-233-389C-3

Query Match 93.3%; Score 611; DB 1; Length 188;
Best Local Similarity 91.2%; Pred. No. 2.6e-67;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKWKNKALSRGKRELRMSSSYPTGLADVAKGAPQTLIRPQDMKGASRSPE 60
DB 22 ARLDVASEFRKKWKNKALSRGKRELRMSSSYPTGLADVAKGAPQTLIRPQDMKGASRSPE 81
QY 61 DSSPDARIRKRYROSMMNFGILRSFGCGRFGCTGYOKLAHQIYQFTDKDKDNVAPRSKI 120
DB 82 ASIPDARIRKRYROSMMNFGILRSFGCGRFGCTGYOKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPQGY 125
DB 142 SPQGY 146

RESULT 6
US-08-801-863-3
Sequence 3, Application US/08801863
Patent No. 5810703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JR., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-801-863-3

Query Match 93.3%; Score 611; DB 2; Length 188;
Best Local Similarity 91.2%; Pred. No. 2.6e-67;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKWKNKALSRGKRELRMSSSYPTGLADVAKGAPQTLIRPQDMKGASRSPE 60

Db 22 ARLDVAEERKKKMKWALSRGKRELRLSSSYPTGIADLKAGPAOTVIRPDVGSSRSPO 81
QY 61 DSSPDAARIRVKRYROSNNFQGLRSFGCRFGCTGVOKLAHQIYQFTDKDKDNVAPRSKI 120
Db 82 ASIPDAARIRVKRYROSNNFQGLRSFGCRFGCTGVOKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPQGY 125
Db 142 SPQGY 146

RESULT 7

US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELEPHONE: (212) 596-9000
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-3

Query Match 93.3%; Score 611; DB 2; Length 188;
Best Local Similarity 91.2%; Pred. No. 2.6e-67;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKKMKWALSRGKRELRLSSSYPTGIADLVKAGPAOTLIRPDMKGASRPE 60
Db 22 ARLDVAEERKKKMKWALSRGKRELRLSSSYPTGIADLKAGPAOTVIRPDVGSSRSPO 81
QY 61 DSSPDAARIRVKRYROSNNFQGLRSFGCRFGCTGVOKLAHQIYQFTDKDKDNVAPRSKI 120
Db 82 ASIPDAARIRVKRYROSNNFQGLRSFGCRFGCTGVOKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPQGY 125
Db 142 SPQGY 146

RESULT 8
US-09-004-713-3

; Sequence 3, Application US/09004713

; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-3

Query Match 93.3%; Score 611; DB 2; Length 188;
Best Local Similarity 91.2%; Pred. No. 2.6e-67;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKKMKWALSRGKRELRLSSSYPTGIADLVKAGPAOTLIRPDMKGASRPE 60
Db 22 ARLDVAEERKKKMKWALSRGKRELRLSSSYPTGIADLKAGPAOTVIRPDVGSSRSPO 81
QY 61 DSSPDAARIRVKRYROSNNFQGLRSFGCRFGCTGVOKLAHQIYQFTDKDKDNVAPRSKI 120
Db 82 ASIPDAARIRVKRYROSNNFQGLRSFGCRFGCTGVOKLAHQIYQFTDKDKDNVAPRSKI 141
QY 121 SPQGY 125
Db 142 SPQGY 146

RESULT 9
US-09-070-504-14

; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muelting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN


```

; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180,00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-070-504-14

Query Match          43.2%; Score 283; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.4e-28;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 YROSNNFQGLRSGFCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPGY 125
DB 1 YROSNNFQGLRSGFCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 10
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueling, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180,00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-070-504-15

Query Match          35.3%; Score 231; DB 4; Length 50;
Best Local Similarity 84.6%; Pred. No. 1.9e-21;
Matches 44; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 74 YROSNNFQGLRSGFCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPGY 125
DB 1 YROSNNFQGLRSGFCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPGY 50

RESULT 11
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueling, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180,00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-070-504-23

Query Match          24.9%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 125
DB 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

RESULT 12
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
```

```

;
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-42020US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: P072
; OTHER INFORMATION: PreproAM(116-146)
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; US-09-011-922A-3
;
; Query Match 24.9%; Score 163; DB 4; Length 31;
; Best Local Similarity 100.0%; Pred. No. 2,2e-13;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 95 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 125
; DB 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
;
; RESULT 13
; US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17

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;
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-42020US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
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; US-09-011-922A-14
;
; Query Match 24.9%; Score 163; DB 4; Length 31;
; Best Local Similarity 100.0%; Pred. No. 2,2e-13;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 95 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 125
; DB 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
;
; RESULT 14
; US-09-011-922A-7
; Sequence 7, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17

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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10154-0053
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: MS WORD 97
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/011,922A
;; FILING DATE: 17-Feb-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/60/002,514
;; FILING DATE: 18-Aug-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/60/002,936
;; FILING DATE: 30-Aug-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/60/013,172
;; FILING DATE: 12-Mar-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/13286
;; FILING DATE: 16-Aug-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Leslie A. Serunian
;; REGISTRATION NUMBER: 35,353
;; REFERENCE/DOCKET NUMBER: 2026-42020S3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: No
;; FRAGMENT TYPE: N-terminal
;; FEATURE:
;; NAME/KEY: PAMP-20
;; OTHER INFORMATION: Proadrenomedullin N-
;; OTHER INFORMATION: terminal 20 peptide
;; US-09-011-922A-7
;;
Query Match 16.3%; Score 107; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARLDVASEFRKKKKWALS 20
DB 1 ARLDVASEFRKKKKWALS 20
;;
RESULT 15
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,249A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/864,475
;; FILING DATE: 06-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/681,702
;; FILING DATE: 04-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 00786/071003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 591 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-468-249A-20
;;
Query Match 11.5%; Score 75; DB 2; Length 591;
Best Local Similarity 32.5%; Pred. No. 0.72;
Matches 25; Conservative 12; Mismatches 26; Indels 14; Gaps 5;
QY 4 DVASEFRKKKKWALSRG-KRELRM-SSSP-----TGLADY--KAG---PAQTLRP 49
DB 465 EVQAEIRKSMRWTLALDPKRAKRGSSSYSGPMVSHSYVNVGPRAGLSIPSLRPP 524
QY 50 QPMKASRSPEDSSPDA 66
DB 525 ATTNHSHSLPGHAKPGA 541

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Job time : 8.55049 secs

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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 12.4495 Seconds
(without alignments)
357.079 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185
Perfect score: 947
Sequence: 1 VSVAMYLGLSLAFLGADTAR.....SKPOAHGAPAPPSGSAFEL 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	947	100.0	185	1 US-08-233-389C-1	Sequence 1, Appli
2	947	100.0	185	2 US-08-801-863-1	Sequence 1, Appli
3	947	100.0	185	2 US-08-486-596A-1	Sequence 1, Appli
4	947	100.0	185	2 US-09-004-713-1	Sequence 1, Appli
5	817	86.3	188	1 US-08-233-389C-3	Sequence 3, Appli
6	817	86.3	188	2 US-08-801-863-3	Sequence 3, Appli
7	817	86.3	188	2 US-08-486-596A-3	Sequence 3, Appli
8	817	86.3	188	2 US-09-004-713-3	Sequence 3, Appli
9	283	29.9	52	4 US-09-070-504-14	Sequence 14, Appli
10	231	24.4	50	4 US-09-070-504-15	Sequence 15, Appli
11	163	17.2	31	4 US-09-070-504-23	Sequence 23, Appli
12	163	17.2	31	4 US-09-011-922A-3	Sequence 3, Appli
13	163	17.2	31	4 US-09-011-922A-14	Sequence 14, Appli
14	107	11.3	20	4 US-09-011-922A-7	Sequence 7, Appli
15	86.5	9.1	401	4 US-09-390-721-2	Sequence 2, Appli
16	80	8.4	496	2 US-08-949-637-2	Sequence 2, Appli
17	80	8.4	496	4 US-09-291-488-2	Sequence 2, Appli
18	79	8.3	450	1 US-08-444-734A-8	Sequence 8, Appli
19	78	8.2	450	1 US-08-194-338-5	Sequence 5, Appli
20	76.5	8.1	490	1 US-08-472-028A-10	Sequence 10, Appli
21	76.5	8.1	490	4 US-09-071-296-10	Sequence 10, Appli
22	76.5	8.1	490	4 US-09-196-268-10	Sequence 10, Appli
23	76.5	8.1	490	4 US-09-015-683-10	Sequence 10, Appli
24	76.5	8.1	490	4 US-09-191-998-10	Sequence 10, Appli
25	76	8.0	373	4 US-09-039-198A-14	Sequence 14, Appli
26	76	8.0	373	4 US-09-039-198A-15	Sequence 15, Appli
27	76	8.0	387	2 US-08-486-839-6	Sequence 6, Appli

28	76	8.0	387	3 US-09-151-011-6	Sequence 6, Appli
29	76	8.0	387	4 US-09-343-623-6	Sequence 6, Appli
30	76	8.0	410	1 US-07-945-283-4	Sequence 4, Appli
31	76	8.0	466	2 US-08-486-839-4	Sequence 4, Appli
32	76	8.0	466	3 US-09-151-011-4	Sequence 4, Appli
33	76	8.0	466	4 US-09-039-198A-2	Sequence 2, Appli
34	76	8.0	466	4 US-09-039-198A-4	Sequence 4, Appli
35	76	8.0	466	4 US-09-343-623-4	Sequence 4, Appli
36	75	7.9	591	2 US-08-468-249A-20	Sequence 20, Appli
37	74.5	7.9	933	4 US-08-764-870-14	Sequence 14, Appli
38	74.5	7.9	933	4 US-08-980-115-14	Sequence 14, Appli
39	74	7.8	302	2 US-08-893-853-3	Sequence 3, Appli
40	74	7.8	302	4 US-09-113-921-3	Sequence 3, Appli
41	73.5	7.8	1323	1 US-08-026-138E-4	Sequence 4, Appli
42	72	7.6	434	1 US-08-337-602-2	Sequence 2, Appli
43	72	7.6	434	3 US-08-558-135-2	Sequence 2, Appli
44	72	7.6	2336	4 US-09-268-163-10	Sequence 10, Appli
45	70	7.4	423	4 US-08-939-366-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855

; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,389C
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-233-389C-1

Query Match 100.0%; Score 947; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSVAMYLGLSLAFLGADTARLDVASEFRKKWNKWLASRGKRELMSSTSSYPTGLADYKAGP 60
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DB 4 VSVAMYLGLSLAFLGADTARLDVASEFRKKWNKWLASRGKRELMSSTSSYPTGLADYKAGP 63

QY 61 AQTLLRPQDMKGASRSPDSSPDAAIRIVKRYRQSMNMFQGLRSGCRFGTCTVQKLAHQ 120
DB 64 AQTLLRPQDMKGASRSPDSSPDAAIRIVKRYRQSMNMFQGLRSGCRFGTCTVQKLAHQ 123
QY 121 IYQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPKQAHGAPAPPSGSAPH 180
DB 124 IYQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPKQAHGAPAPPSGSAPH 183
QY 181 FL 182
DB 184 FL 185
RESULT 2
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801.863
; FILING DATE: CURRENTLY HEREWITH
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-1
Query Match 100.0%; Score 947; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSVAMLYLGSFLAFLGADTARLDVASEFRKKWNKVALSRGKRELRLMSSSYPTGLADVKAGP 60
DB 4 VSVAMLYLGSFLAFLGADTARLDVASEFRKKWNKVALSRGKRELRLMSSSYPTGLADVKAGP 63
QY 61 AQTLLRPQDMKGASRSPDSSPDAAIRIVKRYRQSMNMFQGLRSGCRFGTCTVQKLAHQ 120
DB 64 AQTLLRPQDMKGASRSPDSSPDAAIRIVKRYRQSMNMFQGLRSGCRFGTCTVQKLAHQ 123
QY 121 IYQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPKQAHGAPAPPSGSAPH 180
DB 124 IYQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPKQAHGAPAPPSGSAPH 183
QY 181 FL 182
DB 184 FL 185

DB 184 FL 185
RESULT 3
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-1
Query Match 100.0%; Score 947; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSVAMLYLGSFLAFLGADTARLDVASEFRKKWNKVALSRGKRELRLMSSSYPTGLADVKAGP 60
DB 4 VSVAMLYLGSFLAFLGADTARLDVASEFRKKWNKVALSRGKRELRLMSSSYPTGLADVKAGP 63
QY 61 AQTLLRPQDMKGASRSPDSSPDAAIRIVKRYRQSMNMFQGLRSGCRFGTCTVQKLAHQ 120
DB 64 AQTLLRPQDMKGASRSPDSSPDAAIRIVKRYRQSMNMFQGLRSGCRFGTCTVQKLAHQ 123
QY 121 IYQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPKQAHGAPAPPSGSAPH 180
DB 124 IYQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPKQAHGAPAPPSGSAPH 183
QY 181 FL 182
DB 184 FL 185
RESULT 4
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-004-713-1

Query Match 100.0%; Score 947; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSVAMYLGLSLAFLGADTARLDVASEFRKKNKVALSRGKRELMSSTPTGLADVKAGP 60
DB 4 VSVAMYLGLSLAFLGADTARLDVASEFRKKNKVALSRGKRELMSSTPTGLADVKAGP 63
QY 61 AQTLLRPQDMKGASRPDSFPAARIRVKRYQSMNMFQGLRSGFRGCTCTVQKLAHQ 120
DB 64 AQTLLRPQDMKGASRPDSFPAARIRVKRYQSMNMFQGLRSGFRGCTCTVQKLAHQ 123
QY 121 IYQFTDKDKNVAPRSKISPGYGRRRRSLPEAGPGRTLVSSKPOAHGAPAPPSGAPH 180
DB 124 IYQFTDKDKNVAPRSKISPGYGRRRRSLPEAGPGRTLVSSKPOAHGAPAPPSGAPH 183
QY 181 FL 182
DB 184 FL 185
RESULT 5
US-08-233-389C-3
Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-233-389C-3
Query Match 86.3%; Score 817; DB 1; Length 188;
Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 VSVAMYLGLSLAFLGADTARLDVASEFRKKNKVALSRGKRELMSSTPTGLADVKAGP 60
DB 4 VSVAMYLGLSLAFLGADTARLDVASEFRKKNKVALSRGKRELMSSTPTGLADVKAGP 63
QY 61 AQTLLRPQDMKGASRPDSFPAARIRVKRYQSMNMFQGLRSGFRGCTCTVQKLAHQ 120
DB 64 AQTLLRPQDMKGASRPDSFPAARIRVKRYQSMNMFQGLRSGFRGCTCTVQKLAHQ 123
QY 121 IYQFTDKDKNVAPRSKISPGYGRRRRSLPEAGPGRTLVSSKPOAHGAPAPPS 175
DB 124 IYQFTDKDKNVAPRSKISPGYGRRRRSLPEAGPGRTLVSSKPOAHGAPAPPS 178
RESULT 6
US-08-801-863-3
Sequence 3, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-3
Query Match      86.3%; Score 817; DB 2; Length 188;
Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VSVALMYLGLSLAFLGADTARLDVASEFRKKWKNWALSRRKRELMSSSYPTGLADVKAGP 60
Db 4 VPVALMYLGLSLAFLGADTARLDVAAEFRKKWKNWALSRRKRELRLSSSYPTGTIADLKAGP 63
Qy 61 AQTILRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNMFQGLRSFCRGFTCTVQKLAHQ 120
Db 64 AQTILRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNMFQGLRSFCRGFTCTVQKLAHQ 123
Qy 121 IYQFTDKDKDNVAPRSKISPGYGRRRRRSLPEAGPGRITLVSSKPOAHGAPAPPS 175
Db 124 IYQFTDKDKDNVAPRSKISPGYGRRRRRSLPEASLGRITLVSSKPOAHGAPAPSPA 178

RESULT 8
US-09-004-713-3
; Sequence 3, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: C/O FISH & NEAVE
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-004-713-3
Query Match      86.3%; Score 817; DB 2; Length 188;
Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VSVALMYLGLSLAFLGADTARLDVASEFRKKWKNWALSRRKRELMSSSYPTGLADVKAGP 60
Db 4 VPVALMYLGLSLAFLGADTARLDVAAEFRKKWKNWALSRRKRELRLSSSYPTGTIADLKAGP 63
Qy 61 AQTILRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNMFQGLRSFCRGFTCTVQKLAHQ 120
Db 64 AQTILRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNMFQGLRSFCRGFTCTVQKLAHQ 123
Qy 121 IYQFTDKDKDNVAPRSKISPGYGRRRRRSLPEAGPGRITLVSSKPOAHGAPAPPS 175
Db 124 IYQFTDKDKDNVAPRSKISPGYGRRRRRSLPEASLGRITLVSSKPOAHGAPAPSPA 178
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-3
Query Match      86.3%; Score 817; DB 2; Length 188;
Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VSVALMYLGLSLAFLGADTARLDVASEFRKKWKNWALSRRKRELMSSSYPTGLADVKAGP 60
Db 4 VPVALMYLGLSLAFLGADTARLDVAAEFRKKWKNWALSRRKRELRLSSSYPTGTIADLKAGP 63
Qy 61 AQTILRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNMFQGLRSFCRGFTCTVQKLAHQ 120
Db 64 AQTILRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNMFQGLRSFCRGFTCTVQKLAHQ 123
Qy 121 IYQFTDKDKDNVAPRSKISPGYGRRRRRSLPEAGPGRITLVSSKPOAHGAPAPPS 175
Db 124 IYQFTDKDKDNVAPRSKISPGYGRRRRRSLPEASLGRITLVSSKPOAHGAPAPSPA 178

RESULT 7
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: C/O FISH & NEAVE
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-596A-3
Query Match      86.3%; Score 817; DB 2; Length 188;
Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
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RESULT 9
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-14

Query Match 29.9%; Score 283; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.6e-25;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 YRQSMNFGLSFGCGFCTCTVQKLAHQIYFTDKDKDNVAPRSKISPGY 143
Db 1 YRQSMNFGLSFGCGFCTCTVQKLAHQIYFTDKDKDNVAPRSKISPGY 52
|||||

RESULT 10
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-15

Query Match 24.4%; Score 231; DB 4; Length 50;
Best Local Similarity 84.6%; Pred. No. 3.8e-19;
Matches 44; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 92 YRQSMNFGLSFGCGFCTCTVQKLAHQIYFTDKDKDNVAPRSKISPGY 143
Db 1 YRQSMN--QGRSRTGCGTCTVQKLAHQIYFTDKDKDGMAPRNKISPGY 50
|||||

RESULT 11
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

Query Match 17.2%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 143
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 12

US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.936
; FILING DATE: 30-Aug-1995
; APPLICATION DATA:
; APPLICATION NUMBER: US/60/013.172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: P072
; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

Query Match 17.2%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 143
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 13

US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013.172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

Query Match 17.2%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 143
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 14
US-09-011-922A-7
; Sequence 7, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: PAMP-20
; OTHER INFORMATION: Proadrenomedullin N-
; OTHER INFORMATION: terminal 20 peptide
US-09-011-922A-7

Query Match 11.3%; Score 107; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 ARLDVASEFRKKWKWALS 38
DB 1 ARLDVASEFRKKWKWALS 20

RESULT 15
US-09-390-721-2
; Sequence 2, Application US/09390721
; Patent No. 6197591
; GENERAL INFORMATION:
; APPLICANT: STUTZMAN-ENGWALL, KIM J.
; APPLICANT: PRICE, BRENDA S.
; TITLE OF INVENTION: STREPTOMYCES AVERMITILIS REGULATORY GENES FOR INCREASED
; TITLE OF INVENTION: AVERMECTIN PRODUCTION
; FILE REFERENCE: PC9944A
; CURRENT APPLICATION NUMBER: US/09/390,721
; CURRENT FILING DATE: 1999-09-07
; EARLIER APPLICATION NUMBER: 60/100,134
; EARLIER FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-09-390-721-2

Query Match 9.1%; Score 86.5; DB 4; Length 401;
Best Local Similarity 20.5%; Pred. No. 0.12;
Matches 52; Conservative 26; Mismatches 83; Indels 93; Gaps 8;
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DB 157 SPGLLLIGFAALIGA-----WOLGRAARQRAFAVRAAEQLAQRVTE 199
QY 48 -----SYPTGLADVKAGPAQTL--IRPQDMKGCASRSPEDSSPDAAIRVKRY 92
DB 200 ERLRIARELHDVVTHSMGLTAVKVGVAHVHVRPOEAYDALQVIERTSALTN-DMRRM 258
QY 93 RQSMNNFQGLR---SFGCRFGTCTVOKLAHQ-----IYQFTDKDK 129
DB 259 LGVLTSEGERQSAALGPLFGALPDLVQAGALTMRGVESLPDGVALAVIRIVQEAL 318
QY 130 DNVA-----PRSKISPGYGRRRRSLPEAGPGRTLVSSKPOAHG----- 169
DB 319 TNVAKHAGPEARCRAVDANGHGVRLEITDDGDRSPAPKPGGHGIVGMRRVALYGGT 378
QY 170 ---APAPPSGSAPH 180
DB 379 FAAGPRPEGFAVH 392

Search completed: October 17, 2002, 15:22:04
Job time : 13.4495 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: October 17, 2002, 14:45:20 : Search time 4.53865 Seconds
(without alignments)
279.848 Million cell updates/sec

Title: US-10-018-924-2_COPY_95_146

Perfect score: 283

Sequence: 1 YRQSMNFGFLRSGFCRFGT.....FTDKDKNVAPRSKISPGQY 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	52	4	US-09-070-504-14
2	283	100.0	185	1	US-08-233-389C-1
3	283	100.0	185	2	US-08-801-863-1
4	283	100.0	185	2	US-08-486-596A-1
5	283	100.0	185	2	US-09-004-713-1
6	277	97.9	188	1	US-08-233-389C-3
7	277	97.9	188	2	US-08-801-863-3
8	277	97.9	188	2	US-08-486-596A-3
9	277	97.9	188	2	US-09-004-713-3
10	231	81.6	50	4	US-09-070-504-15
11	163	57.6	31	4	US-09-070-504-23
12	163	57.6	31	4	US-09-011-922A-3
13	163	57.6	31	4	US-09-011-922A-14
14	57	20.1	13	4	US-09-011-922A-2
15	56	19.8	858	2	US-08-265-628-2
16	53	18.7	508	1	US-07-891-942G-10
17	53	18.7	529	1	US-07-891-942G-8
18	53	18.7	529	2	US-08-370-909-19
19	53	18.7	529	2	US-08-504-048-8
20	53	18.7	537	4	US-08-540-922D-12
21	53	18.7	560	1	US-07-891-942G-5
22	52	18.4	775	2	US-08-966-388-4
23	52	18.4	775	3	US-09-188-403-4
24	52	18.4	775	4	US-09-188-404-4
25	52	18.4	775	4	US-09-281-259-4
26	51	18.0	10	2	US-08-934-222-17
27	51	18.0	10	2	US-08-933-402-17

28	51	18.0	10	2	US-09-207-621-17	Sequence 17, Appl
29	51	18.0	10	2	US-08-532-818-17	Sequence 17, Appl
30	51	18.0	10	3	US-09-231-797-17	Sequence 17, Appl
31	51	18.0	10	3	US-08-934-224-17	Sequence 17, Appl
32	51	18.0	10	3	US-08-933-843-17	Sequence 17, Appl
33	51	18.0	10	4	US-08-934-223-17	Sequence 17, Appl
34	51	18.0	10	4	US-09-413-492-17	Sequence 17, Appl
35	51	18.0	1261	4	US-09-439-313-538	Sequence 538, App
36	50	17.7	364	1	US-08-318-831-6	Sequence 6, Appl
37	50	17.7	423	2	US-08-290-731C-10	Sequence 10, Appl
38	50	17.7	1319	2	US-08-290-731C-2	Sequence 2, Appl
39	50	17.7	1333	3	US-09-356-952-2	Sequence 2, Appl
40	50	17.7	1336	2	US-08-290-731C-6	Sequence 6, Appl
41	49	17.3	630	2	US-08-797-366-3	Sequence 3, Appl
42	49	17.3	630	2	US-08-956-268-3	Sequence 29, Appl
43	48	17.0	138	1	US-08-470-179-29	Sequence 23, Appl
44	47.5	16.8	795	3	US-09-031-563-23	Sequence 9, Appl
45	47	16.6	430	2	US-08-290-731C-9	

ALIGNMENTS

RESULT 1
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saba, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-14

Query Match 100.0%; Score 283; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 8e+35;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 YRQSMNFGFLRSGFCRFGTCTVQKLAHQIYQFTDKDKNVAPRSKISPGQY 52
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801.863
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-1

Query Match 100.08; Score 283; DB 2; Length 185;
Best Local Similarity 100.08; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0; Indels 0

QY 1 YRSMNMFGLRSFGRCFTCTVQKLAHQIYFTDKDNDVAPRSKISPGQY 52
   |||||||
Db 95 YRSMNMFGLRSFGRCFTCTVQKLAHQIYFTDKDNDVAPRSKISPGQY 146
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RESULT 4
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-596A-1

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Query Match      100.0%; Score 283; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YROSMNFGQLRSFGCRGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
Db 95 YROSMNFGQLRSFGCRGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 5
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-1

Query Match      100.0%; Score 283; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YROSMNFGQLRSFGCRGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
Db 95 YROSMNFGQLRSFGCRGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 6
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-3

Query Match          97.9%; Score 277; DB 2; Length 188;
Best Local Similarity 98.1%; Pred. No. 3e-33;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRQSMNFFOGLRSGCRFGCTGVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 52
Db 95 YRQSMNFFOGLRSGCRFGCTGVQKLAHQIYQFTDKDKDGVPAPRSKISPGQY 146

RESULT 8
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-3

Query Match          97.9%; Score 277; DB 2; Length 188;
Best Local Similarity 98.1%; Pred. No. 3e-33;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRQSMNFFOGLRSGCRFGCTGVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 52
Db 95 YRQSMNFFOGLRSGCRFGCTGVQKLAHQIYQFTDKDKDGVPAPRSKISPGQY 146

RESULT 9
US-09-004-713-3
; Sequence 3, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-3

Query Match          97.9%; Score 277; DB 2; Length 188;
Best Local Similarity 98.1%; Pred. No. 3e-33;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRQSMNFFOGLRSGCRFGCTGVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 52
Db 95 YRQSMNFFOGLRSGCRFGCTGVQKLAHQIYQFTDKDKDGVPAPRSKISPGQY 146

RESULT 10
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetling, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
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RESULT 13

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US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013.172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14
Query Match 57.6%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52
|
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 14
US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:

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; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013.172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: P071
; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2
Query Match 20.1%; Score 57; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 HQIYQFTDKD 37
|
Db 4 HQIYQFTDKD 13

RESULT 15
US-08-265-628-2
; Sequence 2, Application US/08265628
; Patent No. 5821094
; GENERAL INFORMATION:
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Goring, Daphne
; TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
; TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE

```

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison St. Suite 3400
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,628
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,945
; FILING DATE:
; APPLICATION NUMBER: US 07/847,564
; FILING DATE: 03-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien Ph.D., Donald J.
; REGISTRATION NUMBER: 32,167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-707-8889
; TELEFAX: 312-707-9155
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 858 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-265-628-2

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Query Match      19.8%; Score 56; DB 2; Length 858;
Best Local Similarity 39.5%; Pred. No. 8;
Matches 15; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

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QY      6 NNFQGLRS---FGCRF-GTCTVQKLAHQIYQFTDKDKD 39
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Db     218 NGVGYRSGPWNVGRFGIPEDQKLSYMYNFTDNSEE 255

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Search completed: October 17, 2002, 14:48:43
Job time : 5.53865 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 : Search time 3.49127 Seconds
(without alignments)
279.848 Million cell updates/sec

Title: US-10-018-924-2_COPY_107_146

Perfect score: 219

Sequence: 1 SFGCRFGCTVQKLAHQIYQFTDKDNVAPRSKISPGGY 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	219	100.0	52	4	US-09-070-504-14
2	219	100.0	185	1	US-08-233-389C-1
3	219	100.0	185	2	US-08-801-863-1
4	219	100.0	185	2	US-08-486-596A-1
5	219	100.0	185	2	US-09-004-713-1
6	213	97.3	188	1	US-08-233-389C-3
7	213	97.3	188	2	US-08-801-863-3
8	213	97.3	188	2	US-08-486-596A-3
9	213	97.3	188	2	US-09-004-713-3
10	196	89.5	50	4	US-09-070-504-15
11	163	74.4	31	4	US-09-070-504-23
12	163	74.4	31	4	US-09-011-922A-3
13	163	74.4	31	4	US-09-011-922A-14
14	57	26.0	13	4	US-09-011-922A-2
15	52	23.7	775	2	US-08-966-388-4
16	52	23.7	775	3	US-09-188-403-4
17	52	23.7	775	4	US-09-188-404-4
18	52	23.7	775	4	US-09-281-259-4
19	51	23.3	10	2	US-08-934-222-17
20	51	23.3	10	2	US-08-933-402-17
21	51	23.3	10	2	US-09-207-621-17
22	51	23.3	10	2	US-08-532-818-17
23	51	23.3	10	3	US-09-231-797-17
24	51	23.3	10	3	US-08-934-224-17
25	51	23.3	10	3	US-08-933-843-17
26	51	23.3	10	4	US-08-934-223-17
27	51	23.3	10	4	US-09-413-492-17

28	51	23.3	1261	4	US-09-439-313-538	Sequence 538, Appl
29	50.5	23.1	858	2	US-08-265-628-2	Sequence 2, Appli
30	47	21.5	1477	3	US-08-492-459-10	Sequence 10, Appl
31	47	21.5	1477	3	US-08-423-752-10	Sequence 3, Appli
32	47	21.5	1477	3	US-08-945-994-3	Sequence 24, Appl
33	47	21.5	1477	4	US-08-716-873-24	Sequence 24, Appl
34	47	21.5	1477	4	US-09-368-431-24	Sequence 10, Appl
35	47	21.5	1477	4	US-09-414-006-10	Sequence 10, Appl
36	46.5	21.2	131	4	US-09-247-155-174	Sequence 174, App
37	46	21.0	42	4	US-09-167-681-47	Sequence 47, Appl
38	46	21.0	336	4	US-09-141-206-7	Sequence 7, Appli
39	46	21.0	932	4	US-09-141-206-6	Sequence 6, Appli
40	46	21.0	933	4	US-09-141-206-2	Sequence 2, Appli
41	46	21.0	933	4	US-09-107-149-2	Sequence 2, Appli
42	46	21.0	933	4	US-09-107-149-17	Sequence 17, Appl
43	46	21.0	1622	4	US-08-972-527-6	Sequence 6, Appli
44	45	20.5	932	3	US-08-968-752B-6	Sequence 6, Appli
45	44.5	20.3	148	1	US-08-207-904-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070, 504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-14

Query Match	100.0%;	Score 219;	DB 4;	Length 52;
Best Local Similarity	100.0%;	Pred. No. 3.6e-26;		
Matches	40;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	SFGCRFGCTVQKLAHQIYQFTDKDNVAPRSKISPGGY	40	
Db	13	SFGCRFGCTVQKLAHQIYQFTDKDNVAPRSKISPGGY	52	

१

Query Match 100.0%; Score 219; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 40
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Db 107 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 146

RESULT 5

US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,713
; FILING DATE: JANUARY 7, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-004-713-1

Query Match 100.0%; Score 219; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 40
|||||
Db 107 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 146

RESULT 6

US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE

; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,389C
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-233-389C-3

Query Match 97.3%; Score 213; DB 1; Length 188;
Best Local Similarity 97.5%; Pred. No. 1.3e-24;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 40
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Db 107 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 146

RESULT 7

US-08-801-863-3
; Sequence 3, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,863
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-801-863-3

Query Match 97.3%; Score 213; DB 2; Length 188;
 Best Local Similarity 97.5%; Pred. No. 1.3e-24;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
 Db 107 SFGCRFGCTVQKLAHQIYQFTDKDKDGVAPRSKISPGY 146

RESULT 8
 US-08-486-596A-3
 Sequence 3, Application US/08486596A
 Patent No. 5837823

GENERAL INFORMATION:
 APPLICANT: KITAMURA, Kazuo
 APPLICANT: KANGAWA, Kenji
 APPLICANT: MATSUO, Hisayuki
 APPLICANT: ETO, Tanenao
 TITLE OF INVENTION: ADRENOMEDULLIN
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: C/O FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,596A
 FILING DATE: JUNE 7, 1995
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: HALEY Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-596A-3

Query Match 97.3%; Score 213; DB 2; Length 188;
 Best Local Similarity 97.5%; Pred. No. 1.3e-24;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
 Db 107 SFGCRFGCTVQKLAHQIYQFTDKDKDGVAPRSKISPGY 146

RESULT 9
 US-09-004-713-3
 Sequence 3, Application US/09004713
 Patent No. 5910416

GENERAL INFORMATION:
 APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji
 APPLICANT: MATSUO, Hisayuki
 APPLICANT: ETO, Tanenao
 TITLE OF INVENTION: ADRENOMEDULLIN
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: C/O FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/004,713
 FILING DATE: JANUARY 7, 1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HALEY Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-004-713-3

Query Match 97.3%; Score 213; DB 2; Length 188;
 Best Local Similarity 97.5%; Pred. No. 1.3e-24;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SFGCRFGCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
 Db 107 SFGCRFGCTVQKLAHQIYQFTDKDKDGVAPRSKISPGY 146

RESULT 10
 US-09-070-504-15
 Sequence 15, Application US/09070504
 Patent No. 6268474
 GENERAL INFORMATION:
 APPLICANT: Smith, Derek D.
 APPLICANT: Saha, Shankar
 APPLICANT: Abel, Peter W.
 TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
 STREET: 119 No. 6268474th Fourth Street
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/070,504
 FILING DATE: 30-APR-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14
Query Match 74.4%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TVQKLHQIYQFTDKDNVAPRSKISPGY 40
Db 1 TVQKLHQIYQFTDKDNVAPRSKISPGY 31
RESULT 14
US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide

; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
; FEATURE:
; NAME/KEY: P071
; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2
Query Match 26.0%; Score 57; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 HQIYQFTDKD 25
Db 4 HQIYQFTDKD 13
RESULT 15
US-08-966-388-4
; Sequence 4, Application US/08966388
; Patent No. 5965412
; GENERAL INFORMATION:
; APPLICANT: Tomoyuki NISHIMOTO
; APPLICANT: Michio KUBOTA
; APPLICANT: Hiroto CHAEN
; APPLICANT: Toshio MIYAKE

;; TITLE OF INVENTION: KOTIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEWMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/966,388
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 311,235/1996
;; FILING DATE: 8-NOV-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 61,710/97
;; FILING DATE: 3-MAR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 775 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-966-388-4

Query Match 23.7%; Score 52; DB 2; Length 775;
Best Local Similarity 36.0%; Pred. No. 15;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 15 AHQIYQFTDKDKDNVAPRSKISPGQ 39
Db 217 AVRLYHYEDREKKNIAKFRPLPLG 241

Search completed: October 17, 2002, 14:48:42
Job time : 5.49127 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 ; Search time 12,5786 Seconds
(without alignments)
459.181 Million cell updates/sec

Title: US-10-018-924-2_COPY_95_146

Perfect score: 283

Sequence: 1 YRQSMNPFQGLRSGCRFGT.....FTDKDKDNVAPRSKISPOGY 52

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	52	22 AAB75110	Human adrenomedullin
2	283	100.0	52	22 AAB91759	Adrenomedullin pep
3	283	100.0	52	22 AAE09818	Human adrenomedullin
4	283	100.0	53	22 AAB75111	Glycine extended h
5	283	100.0	53	22 AAB75112	Glycine extended a
6	283	100.0	62	22 AAB75113	Linker peptide-adr
7	283	100.0	120	22 AAB75122	UspA(1-57)-(A)-(GS
8	283	100.0	120	22 AAB75123	UspA(1-56)-(DD)-(G
9	283	100.0	147	22 AAB75124	UspA(1-84)-(A)-(GS
10	283	100.0	170	22 AAB75114	Thioredoxin-(GSGSG
11	283	100.0	185	22 AAB49697	Human adrenomedullin

12	283	100.0	185	22	AAB60344	Human adrenomedullin
13	277	97.9	188	22	AAB49698	Porcine adrenomedu
14	277	97.9	188	22	AAB60345	Porcine adrenomedu
15	231	81.6	50	22	AAE09819	Rat adrenomedullin
16	231	81.6	185	22	AAB49699	Rat adrenomedullin
17	231	81.6	185	22	AAB60346	Rat adrenomedullin
18	227	80.2	52	22	AAB91765	Adrenomedullin pep
19	219.5	77.6	53	22	AAB91767	Adrenomedullin pep
20	196	69.3	40	22	AAB91768	Adrenomedullin pep
21	181.5	64.1	37	22	AAB91761	Adrenomedullin pep
22	163	57.6	31	18	AAW25160	Human preproadreno
23	163	57.6	31	22	AAB91762	Adrenomedullin pep
24	163	57.6	31	22	AAE09827	Human adrenomedullin
25	64	22.6	12	22	AAB91760	Adrenomedullin pep
26	61	21.6	1541	18	AAW33361	Rat canaliculic mu
27	60	21.2	231	21	AAB11449	Human cMOAT C-term
28	60	21.2	231	21	AAB28224	Multi-drug resista
29	60	21.2	1545	18	AAW33362	Human canaliculic
30	59	20.8	1545	19	AAW55966	Human canaliculic
31	57	20.1	13	18	AAW25159	Human preproadreno
32	56.5	20.0	1346	22	ABE65953	Drosophila melanog
33	56	19.8	339	21	AAB26100	Mycobacterium aur
34	56	19.8	339	21	AAB26104	Mycobacterium aur
35	56	19.8	500	22	ABB67015	Drosophila melanog
36	56	19.8	858	15	AAE33404	S-Locus receptor (
37	56	19.8	858	19	AAW49080	Brassica sp. S-rec
38	56	19.8	1302	22	ABE65954	Drosophila melanog
39	55	19.4	297	21	AAE75592	Neisseria gonorrh
40	55	19.4	1344	22	ABE59224	Drosophila melanog
41	54.5	19.3	482	21	AAG14118	Arabidopsis thalia
42	54.5	19.3	482	21	AAG54151	Arabidopsis thalia
43	54.5	19.3	483	21	AAG14117	Arabidopsis thalia
44	54.5	19.3	483	21	AAG54150	Arabidopsis thalia
45	54.5	19.3	490	21	AAG54149	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAB75110	
ID	AAB75110 standard; Protein; 52 AA.
XX	
AC	AAB75110;
XX	
DT	31-JUL-2001 (first entry)
XX	
DE	Human adrenomedullin (AM) protein.
XX	
KW	Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
XX	adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
OS	Homo sapiens.
XX	
PN	WO200127310-A1.
XX	
PD	19-APR-2001.
XX	
PF	10-OCT-2000; 2000WO-JP07023.
XX	
PR	15-OCT-1999; 99JP-0294147.
XX	
PA	(SHIO) SHIONOGI & CO LTD.
XX	
PI	Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX	
DR	WPI: 2001-282044/29.
XX	
DR	N-PSDB; AAH19806.
XX	
PT	Producing adrenomedullin useful for pharmaceutical and diagnostic
XX	application comprises producing fused adrenomedullin precursor using a
PT	recombinant host
XX	

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimide) and maleimide groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

XX	WO200127310-A1.
PN	
XX	19-APR-2001.
XX	
XX	10-OCT-2000; 2000WO-JP07023.
XX	
XX	15-OCT-1999; 99JP-0294147.
PR	
XX	(SHIO) SHIONOGI & CO LTD.
PA	
XX	Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI	
XX	WPI; 2001-282044/29.
DR	N-PSDB; AAH19808.
DR	
XX	Producing adrenomedullin useful for pharmaceutical and diagnostic
PT	application comprises producing fused adrenomedullin precursor using a
PT	recombinant host
XX	
XX	Disclosure; Page 47; 75pp; Japanese.
PS	
XX	The present invention describes a method (M1) for producing
CC	adrenomedullin precursor. The method comprises: (a) producing the fused
CC	protein using a recombinant host cell; (b) restricted digestion of the
CC	fused protein by a protease followed by collection of sediment; and
CC	(c) dissolving the sediment and extracting adrenomedullin precursor.
CC	The method can be used for the production of adrenomedullin precursor
CC	for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC	and AAH75110 to AAH75124 represent sequences which are used in the
CC	exemplification of the present invention.
XX	
XX	Sequence 53 AA;
QQ	
XX	Query Match 100.0%; Score 283; DB 22; Length 53;
XX	Best Local Similarity 100.0%; Pred. No. 2.7e-32;
XX	Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 YRQSMNNFQGLRSGFRGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGGY 52
Db	1 YRQSMNNFQGLRSGFRGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGGY 52
XX	
RESULT 6	
AAH75113	
ID	AAH75113 standard; Protein; 62 AA.
XX	
AC	AAH75113;
XX	
DT	31-JUL-2001 (first entry)
XX	
DE	Linker peptide-adrenomedullin (AM) precursor protein.
XX	
XX	Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW	adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200127310-A1.
XX	
PD	19-APR-2001.
XX	
XX	10-OCT-2000; 2000WO-JP07023.
PF	
XX	15-OCT-1999; 99JP-0294147.
PR	
XX	(SHIO) SHIONOGI & CO LTD.
PA	
XX	Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI	
XX	WPI; 2001-282044/29.
DR	N-PSDB; AAH19809.
DR	

XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX
XX Claim 20; Page 48; 75pp; Japanese.
XX
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
XX Sequence 62 AA;
SQ
Query Match 100.0%; Score 283; DB 22; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e-32;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YROSMNFGRLSFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 52
Db 10 YROSMNFGRLSFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 61
RESULT 7
AAB75122
ID AAB75122 standard; Protein; 120 AA.
XX
XX AAB75122;
XX
XX 31-JUL-2001 (first entry)
XX
XX UsPA(1-57)-(A)-(GSFGDAFE)-AM-gly protein.
XX
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200127310-A1.
XX
XX 19-APR-2001.
XX
XX 10-OCT-2000; 2000WO-JP07023.
XX
XX 15-OCT-1999; 99JP-0294147.
XX
XX (SHIO) SHIONOGI & CO LTD.
XX
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI
XX
XX WPI: 2001-282044/29.
DR N-PSDB; AAH19864.
XX
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX
XX Claim 17; Page 68; 75pp; Japanese.
XX
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the

CC exemplification of the present invention.
XX
XX Sequence 120 AA;
SQ
Query Match 100.0%; Score 283; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.1e-32;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YROSMNFGRLSFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 52
Db 68 YROSMNFGRLSFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 119
RESULT 8
AAB75123
ID AAB75123 standard; Protein; 120 AA.
XX
XX AAB75123;
XX
XX 31-JUL-2001 (first entry)
XX
XX UsPA(1-56)-(DD)-(GSFGDAFE)-AM-gly protein.
XX
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200127310-A1.
XX
XX 19-APR-2001.
XX
XX 10-OCT-2000; 2000WO-JP07023.
XX
XX 15-OCT-1999; 99JP-0294147.
XX
XX (SHIO) SHIONOGI & CO LTD.
XX
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI
XX
XX WPI: 2001-282044/29.
DR N-PSDB; AAH19865.
XX
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX
XX Claim 17; Page 69-70; 75pp; Japanese.
XX
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
XX Sequence 120 AA;
SQ
Query Match 100.0%; Score 283; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.1e-32;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YROSMNFGRLSFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 52
Db 68 YROSMNFGRLSFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 119
RESULT 9
AAB75124

XX	19-APR-2001.
XX	PD
XX	XX
XX	10-OCT-2000; 200WO-JP07023.
XX	PF
XX	XX
XX	15-OCT-1999; 99JP-0294147.
XX	PR
XX	PA
XX	(SHIO) SHIONOGI & CO LTD.
XX	PI
XX	Takimoto A, Mitsuda Y, Nakayama T, Mitsuishima K;
DR	WPI; 2001-282044/29.
DR	N-PSDB; AAH19810.
XX	XX
XX	Producing adrenomedullin useful for pharmaceutical and diagnostic
PT	application comprises producing fused adrenomedullin precursor using a
PT	recombinant host
PT	Claim 17; Page 49-50; 75pp; Japanese.
XX	XX
XX	The present invention describes a method (M1) for producing
CC	adrenomedullin precursor. The method comprises: (a) producing the fused
CC	protein using a recombinant host cell; (b) restricted digestion of the
CC	fused protein by a protease followed by collection of sediment; and
CC	(c) dissolving the sediment and extracting adrenomedullin precursor.
CC	The method can be used for the production of adrenomedullin precursor
CC	for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC	and AAB75110 to AAB75124 represent sequences which are used in the
CC	exemplification of the present invention.
XX	XX
SQ	Sequence 170 AA;
Query Match	100.0%; Score 283; DB 22; Length 170;
Best Local Similarity	100.0%; Pred. No. 1.le-31;
Matches	52; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 YRQSMNFFGLRSFGCGFCTCTVOKLAHQIYQFTDKDKNVAPRSKISPOGY 52
Dd	118 YRQSMNFFGLRSFGCGFCTCTVOKLAHQIYQFTDKDKNVAPRSKISPOGY 169
RESULT 11	
AAB49697	
ID	AAB49697 standard; Protein; 185 AA.
XX	AC
XX	AAB49697;
XX	XX
DT	04-APR-2001 (first entry)
XX	XX
DE	Human adrenomedullin amino acid sequence.
XX	XX
KW	Passive elongation; vesicle smooth muscle; uropathic activity;
KW	adrenomedullin; urinary disorder; incontinence; human.
XX	OS
OS	Homo sapiens.
PX	WO200078338-A1.
PN	XX
PD	28-DEC-2000.
XX	XX
XX	23-JUN-2000; 2000WO-JP04166.
PF	XX
XX	XX
PR	23-JUN-1999; 99JP-0177549.
XX	XX
PA	(SHIO) SHIONOGI & CO LTD.
XX	XX
PI	Yanagita T;
XX	XX
XX	WPI; 2001-080754/09.
DR	DR
DR	N-PSDB; AAF29138.
XX	XX
XX	Composition for promoting passive elongation of vesicle smooth muscle
PT	comprises adrenomedullin -

```

XX PS Claim 1; Page 26-27; 42pp; Japanese.
XX CC This invention relates to a composition for promoting passive elongation
XX CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
XX CC uterine contraction activity. The composition can be used for promoting passive
XX CC elongation of vesicle smooth muscles, this is useful for relieving
XX CC urinary disorders such as impending urinary incontinence, reflex urinary
XX CC incontinence and urinary incontinence with overflow. The present sequence
XX CC represents the human adrenomedullin protein, which is used in the
XX CC composition of the invention.
XX SQ Sequence 185 AA;

Query Match 100.0%; Score 283; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRQSMNFGQLRSGRCFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGGY 52
Db 95 YRQSMNFGQLRSGRCFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGGY 146

RESULT 12
AAB60344
ID AAB60344 standard; Protein; 185 AA.
AC AAB60344;
XX DT 06-APR-2001 (first entry)
XX DE Human adrenomedullin precursor.
XX KW Human; adrenomedullin; precursor; bradykinin antagonist;
XX KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
XX KW dysmenorrhea; obstetric; gynaecological.
XX OS Homo sapiens.
XX PN WO200078339-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-JP04167.
XX PR 23-JUN-1999; 95JP-0177548.
XX PR 21-MAR-2000; 2000JP-0079171.
XX PA (SHIO ) SHIONOGI & CO LTD.
XX PI Yanagita T;
XX DR WPI: 2001-080755/09.
XX DR N-PSDB; AAF27228.
XX CC Composition for inhibiting automatic uterine contraction or contraction
XX CC caused by bradykinin comprises adrenomedullin.
XX PS Claim 7; Page 37-38; 54pp; Japanese.
XX CC The invention relates to a composition containing adrenomedullin for
XX CC inhibiting automatic uterine contraction or contraction caused by
XX CC bradykinin. The invention also relates to the use of adrenomedullin in
XX CC the preparation of a drug for preventing premature birth or miscarriage.
XX CC The composition of the invention can be used for preventing premature
XX CC birth, preventing miscarriage, stopping delivery before caesarean
XX CC section or for treating dysmenorrhea. The present sequence
XX CC represents human adrenomedullin precursor.
XX SQ Sequence 185 AA;

Query Match 100.0%; Score 283; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;

```

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Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRQSMNFGQLRSGRCFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGGY 52
Db 95 YRQSMNFGQLRSGRCFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGGY 146

RESULT 13
AAB49698
ID AAB49698 standard; Protein; 188 AA.
XX AC AAB49698;
XX DT 04-APR-2001 (first entry)
XX DE Porcine adrenomedullin amino acid sequence.
XX KW Passive elongation; vesicle smooth muscle; uropathic activity;
XX KW adrenomedullin; urinary disorder; incontinence; procine.
XX OS Sus scrofa.
XX PN WO200078338-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-JP04166.
XX PR 23-JUN-1999; 99JP-0177549.
XX PA (SHIO ) SHIONOGI & CO LTD.
XX PI Yanagita T;
XX DR WPI: 2001-080754/09.
XX DR N-PSDB; AAF29139.
XX CC Composition for promoting passive elongation of vesicle smooth muscle
XX CC comprises adrenomedullin.
XX PS Disclosure; Page 31-33; 42pp; Japanese.
XX CC This invention relates to a composition for promoting passive elongation
XX CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
XX CC uterine contraction activity. The composition can be used for promoting passive
XX CC elongation of vesicle smooth muscles, this is useful for relieving
XX CC urinary disorders such as impending urinary incontinence, reflex urinary
XX CC incontinence and urinary incontinence with overflow. The present sequence
XX CC represents the porcine adrenomedullin protein, which is used in the
XX CC composition of the invention.
XX SQ Sequence 188 AA;

Query Match 97.9%; Score 277; DB 22; Length 188;
Best Local Similarity 98.1%; Pred. No. 8.4e-31;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRQSMNFGQLRSGRCFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGGY 52
Db 95 YRQSMNFGQLRSGRCFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGGY 146

RESULT 14
AAB60345
ID AAB60345 standard; Protein; 188 AA.
XX AC AAB60345;
XX DT 06-APR-2001 (first entry)
XX DE Porcine adrenomedullin precursor.
XX KW Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;

```


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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 ; Search time 5.96509 Seconds
(without alignments)
837.648 Million cell updates/sec

Title: US-10-018-924-2_COPY_95_146

Perfect score: 283

Sequence: 1 YRQSMNPFQGLRSGREGT.....FTDKDKDNVAPRSKISPGQY 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283	100.0	185	2 JN0684	adrenomedullin pre
2	277	97.9	188	2 S41600	adrenomedullin - p
3	231	81.6	185	2 JN0766	adrenomedullin pre
4	65.5	23.1	532	2 JCI392	monophenol monooxy
5	61.5	21.7	430	2 T14536	S-locus-specific g
6	61	21.6	1541	1 S71839	canalicular multidi
7	60.5	21.4	253	2 H81690	conserved hypothet
8	59	20.8	1545	1 S71841	multidrug resistan
9	58.5	20.7	189	2 A99638	hypothetical prote
10	58.5	20.7	189	2 A85489	hypothetical prote
11	58.5	20.7	431	2 T14415	S-locus-specific g
12	57.5	20.3	429	2 T07809	S-receptor kinase
13	57.5	20.3	712	2 AG2058	ABC transporter AT
14	57	20.1	273	2 PC4153	monophenol monooxy
15	56	19.8	428	2 T14529	S-locus-specific g
16	56	19.8	858	1 JQ1677	S-receptor kinase
17	55.5	19.6	373	2 G84107	lipopolysaccharide
18	55.5	19.6	465	2 T15540	hypothetical prote
19	55	19.4	319	2 S20799	hypothetical prote
20	55	19.4	444	1 E69130	histidine--trNA li
21	54.5	19.3	93	2 E91004	hypothetical prote
22	54.5	19.3	93	2 E85637	hypothetical prote
23	54.5	19.3	428	2 T07814	S-locus-specific g
24	54.5	19.3	436	2 A27827	S-locus-specific g
25	54.5	19.3	463	2 T46165	pectate lyase-like
26	54	19.1	370	2 T05598	hypothetical prote
27	54	19.1	429	2 T14533	S-locus-specific g
28	53.5	18.9	107	2 H84839	late embryogenesis
29	53.5	18.9	358	2 H95398	probable ABC trans

ALIGNMENTS

RESULT 1

JN0684

adrenomedullin precursor - human

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000

C:Accession: J02351; JN0684; P0548; JN0476

R:Shimizu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, H.; Kitamura, K.; Eto,

Biochem. Biophys. Res. Commun. 203, 631-639, 1994

A:Title: Genomic structure of human adrenomedullin gene.

A:Reference number: J02351; MUID:94354869

A:Accession: J02351

A:Molecule type: DNA

A:Residues: 1-185 <ISH>

A:Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330

A:Experimental source: pheochromocytoma

R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.

Biochem. Biophys. Res. Commun. 194, 720-725, 1993

A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome

A:Reference number: JN0684; MUID:93343928

A:Accession: JN0684

A:Molecule type: mRNA

A:Residues: 1-185 <KIT>

A:Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612

A:Accession: P0548

A:Molecule type: protein

A:Residues: 22-41 <KIT>

R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,

Biochem. Biophys. Res. Commun. 192, 553-560, 1993

A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocytoma

A:Reference number: JN0476; MUID:93249425

A:Accession: JN0476

A:Molecule type: protein

A:Residues: 95-146 <KIT>

A:Experimental source: pheochromocytoma

C:Genetics:

A:Gene: GDB:ADM

A:Cross-references: GDB:217070; OMIM:103275

A:Map position: lipter-llqter

A:Introns: 33/2; 83/2

C:Keywords: amidated carboxyl end; blood pressure control; hormone

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-185/Product: proadrenomedullin #status predicted <PEU>

F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>

F:95-146/Product: adrenomedullin #status experimental <NAR>

F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:110-115/Modified site: amidated carboxyl end (Arg) (amide in mature form from following

F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 100.0%; Score 283; DB 2; Length 185;

Best Local Similarity 100.0%; Pred. No. 4.7e-30;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 YRQSMNFGQLRSFCRGFTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
|||||
Db 95 YRQSMNFGQLRSFCRGFTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 2
S41600
adrenomedullin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S41600
R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A:Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encod
A:Reference number: S41600; MUID:94139945
A:Accession: S41600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-188 <KIT>
A:Cross-references: GB:DI4875; NID:g439721; PIDN:BAA03590.1; PID:g496379

Query Match 97.9%; Score 277; DB 2; Length 188;
Best Local Similarity 98.1%; Pred. No. 3e-29;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRQSMNFGQLRSFCRGFTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
|||||
Db 95 YRQSMNFGQLRSFCRGFTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 3
JN0766
adrenomedullin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C:Accession: JN0766; PN0610
R:Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, H.; Eto, T.
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A:Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensive
A:Reference number: JN0766; MUID:93384621
A:Accession: JN0766
A:Molecule type: mRNA
A:Residues: 1-185 <SAK>
A:Accession: PN0610
A:Molecule type: protein
A:Residues: 22-41 <SA2>
C:Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C:Keywords: amidated carboxyl end
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:94-143/Product: adrenomedullin #status predicted <MAT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 81.6%; Score 231; DB 2; Length 185;
Best Local Similarity 84.6%; Pred. No. 3.8e-23;
Matches 44; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

Qy 1 YRQSMNFGQLRSFCRGFTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
|||||
Db 94 YRQSMN--QGRSRSTGCRFGTCTMOKLAHQIYQFTDKDKDGMAPRNKISPOGY 143

RESULT 4
JC1392
monophenol monooxygenase (EC 1.14.18.1) - Japanese pond frog
N:Alternate names: tyrosinase
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JC1392; I51169
```

```
R:Takase, M.; Miura, I.; Nakata, A.; Takeuchi, T.; Nishioka, M.
Gene 121, 359-363, 1992
A:Title: Cloning and sequencing of the cDNA encoding tyrosinase of Japanese pond frog
A:Reference number: JC1392; MUID:93077054
A:Accession: JC1392
A:Molecule type: mRNA
A:Residues: 1-532 <TAK>
A:Cross-references: DBJ:DJ2514; NID:g222946; PIDN:BAA02077.1; PID:g222947
R:Miura, I.; Okumoto, H.; Makino, K.; Nakata, A.; Nishioka, M.
Jpn. J. Genet. 70, 79-92, 1995
A:Title: Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculat
A:Reference number: I51169; MUID:95290234
A:Accession: I51169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9, A', 11-277 <MIU>
A:Cross-references: GB:D37779; NID:g809507; PIDN:BAA07034.1; PID:g809508
C:Superfamily: monophenol monooxygenase
C:Keywords: glycoprotein; oxidoreductase; transmembrane protein
F:47,90,115,165,234,294,341,360,375/Blinding site: carbohydrate (Asn) (covalent) #stat
F:47,90,115,165,234,294,341,360,375/Blinding site: carbohydrate (Asn) (covalent) #stat

Query Match 23.1%; Score 65.5; DB 2; Length 532;
Best Local Similarity 33.9%; Pred. No. 1.2;
Matches 20; Conservative 8; Mismatches 18; Indels 13; Gaps 4;

Qy 3 QSMNFGQLRSFCRGFTCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 49
|||||
Db 94 QCQGNFGYNGCGCRFGYGTGNCIVRRNMIRKDFRTAETKDLIAIYLNLA-KHTISP 151

RESULT 5
T14536
S-locus-specific glycoprotein - wild cabbage (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica oleracea (wild cabbage)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: T14536
R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A:Title: Striking sequence similarity in inter- and intra-specific comparisons o f cl
echanism.
A:Reference number: Z18078; MUID:97352858
A:Accession: T14536
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-430 <KUS>
A:Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 21.7%; Score 61.5; DB 2; Length 430;
Best Local Similarity 28.6%; Pred. No. 3.2;
Matches 14; Conservative 12; Mismatches 12; Indels 11; Gaps 2;

Qy 15 GCRF-GTCTVQKLAHQIYQFTDKDKD-----NVAPRSKISPOGY 52
|||||
Db 220 GIRFSGIPEKLSYMYNFTENNEVAYTFRTNNISYSLRTVSPRGY 268

RESULT 6
S71839
canicular multidrug resistance protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C:Accession: S71839
R:Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler,
J. Biol. Chem. 271, 15091-15098, 1996
A:Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan
A:Reference number: S71839; MUID:96279006
A:Accession: S71839
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1541 <BUE>
```

A:Accession: S71841
A:Molecule type: mRNA
A:Residues: 1-1545 <KOE>
A:Cross-references: EMBL:X96395; NID:q1507819; PIDN:CAA65259.1; PID:q1514568
P:Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, J. Biol. Chem. 271, 15091-15098, 1996
A:Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance protein
A:Reference number: S71839; MUID:96279006
A:Accession: S71840
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1415-1429, 'VP', 1432-1455, 'E', 1457-1545 <BUE>
A:Cross-references: EMBL:X96395
C:Genetics:
A:Gene: GDB:ABCC2; CMOAT; ABC; MRP2; CMRP; DJS
A:Cross-references: GDB:6089489; OMIM:601107
A:Map position: 10q24-10q24
C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C:Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F:634-837/Domain: ATP-binding cassette homology <ABC1>
F:671-678/Region: nucleotide-binding motif A (P-loop)
F:1317-1510/Domain: ATP-binding cassette homology <ABC2>
F:1334-1341/Region: nucleotide-binding motif A (P-loop)

Query Match 20.88; Score 59; DB 1; Length 1545;
Best Local Similarity 37.88; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Qy 18 FGCTVOKLAHQIYQFTDKDKDNVAPRSKI-----SPQ 50
| ||| :||:: | || | || |
Db 1483 FAHCTVTIAHRLHTINDSKVMVLNDNGKIEGCSPE 1519

RESULT 9
A99638
hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain C)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: A99638
P:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; gasawara, N.; Yasunaga, T.; Shiba, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and G
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A99638
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA033496.1; PID:q13359529; GSPDB:GN00154
A:Experimental source: strain O157:H7 substrain E1MD_0500952

C;Genetics:
A;Gene: ECs0073
C;Superfamily: Escherichia coli yabp protein

	Query Match	20.7%	Score 58.5;	DB 2;	Length 189;
	Best Local Similarity	34.4%;	Pred. No. 3.4;		
	Matches 11;	Conservative	9;	Mismatches	7;
				Indels	5;
				Gaps	1;

Qy 25 KLAHQIQFTD-----KDKDNVAPRSKISPG 51
 || : | : | : | : | : | : | : | :
Db 95 KLTHWLKFNELKEYADPNMAAKASLSPEG 126

RESULT 10
A85489
hypothetical protein Z0078 [imported] - Escherichia coli (strain O157:H7, substrain E)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A85489
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamocousis, K.; Apoda
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <STO>
A:Cross-references: GB:A8005174; NID:gl2512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:200145
A:Experimental source: strain Q157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0078
C:Superfamily: Escherichia coli yabP protein

Query Match 20.7%; Score 58.5; DB 2; Length 189;
Best Local Similarity 34.4%; Pred. No. 3.4;
Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

Qy 25 KLRHQIYQFTD-----KQKDNVAPRSKISPOG 51
Db 95 KLTHWLKFNELKEKAKDPENNAKASLSPEC 126

RESULT 11
Ti4415
S:locus-specific glycoprotein - turnip (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica rapa (turnip)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: Ti4415
R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A:Title: Striking sequence similarity in inter- and intra-specific comparisons of a class mechanism.
A:Reference number: 218078; MUID:97352858
A:Accession: Ti4415
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-431 <KUS>
A:Cross-references: EMBL:D85215; NID:g2351161; PIDN:BAA21949.1; PID:g2351162
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 20.7%; Score 58.5; DB 2; Length 431;
Best Local Similarity 32.7%; Pred. No. 7.9;
Matches 16; Conservative 8; Mismatches 14; Indels 11; Gaps 2;

Qy 15 GCRF-GTCTVQKLAHQIYQFTDKD-----NVAPRSKISPOG 52
Db 222 GVRFSGMPGQKLNWVYNFTENSEDVAYTFRTWKNSIYSLKISSEGF 270

RESULT 12
T07809
S:receptor kinase (EC 2.7.1.1) - radish (fragment)
N:Alternate names: S glycoprotein
C:Species: Raphanus sativus (radish)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07809
R:Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A:Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related gene
A:Reference number: 216146; MUID:98311079
A:Accession: T07809
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-429 <SAK>
A:Cross-references: EMBL:AB009677; NID:g3327839; PIDN:BAA31724.1; PID:g3327840
C:Genetics:
A:Gene: SLG(S1)
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: ATP; glycoprotein; magnesium; phosphotransferase; serine/threonine-specific
F:32-427/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match 20.3%; Score 57.5; DB 2; Length 429;
Best Local Similarity 30.0%; Pred. No. 11;

Matches 18; Conservative 10; Mismatches 15; Indels 17; Gaps 3;

Qy 10 GLRSP-----GCRF-GTCTVQKLAHQIYQFTDKD-----NVAPRSKISPOG 52
Db 209 GLRSHSGPWCIGIRSGIPEDOKSSYMYVSTENSEEVAYTFRTWNTSSIYSLKISSEGF 268

RESULT 13
AG2058
ABC transporter ATP-binding protein all2021 [imported] - Anabaena sp. (strain PCC 712
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AG2058
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073720.1; PID:gl7131112; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2021

Query Match 20.3%; Score 57.5; DB 2; Length 712;
Best Local Similarity 37.2%; Pred. No. 18;
Matches 16; Conservative 6; Mismatches 16; Indels 5; Gaps 2;

Qy 9 OGLRSFGCRFGTCTVQKLAHQIYQFTDKDKNVAPRSKISPOG 51
Db 655 QNLRRGC---TCII--VAHRLSTIRDCDQIIVLGRGVVQGS 692

RESULT 14
PC4153
monophenol monooxygenase (EC 1.14.18.1) - chicken
N:Alternate names: tyrosinase
C:Species: Gallus gallus (chicken)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 18-Jun-1999
C:Accession: PC4153
R:Ferguson, C.A.; Kidson, S.H.
Gene 169, 191-195, 1996
A:Title: Characteristic sequences in the promoter region of the chicken tyrosinase-en
A:Reference number: PC4153; MUID:96194800
A:Accession: PC4153
A:Molecule type: DNA
A:Residues: 1-273 <FER>
A:Cross-references: GB:I46805; NID:gl146320; PIDN:AAB08441.1; PID:gl146321
A:Note: The DNA sequence includes the first exon and a part of the first intron
C:Comment: This enzyme is the rate-limiting enzyme in pigment biosynthesis.
C:Genetics:
A:Gene: ctyr4.3
C:Superfamily: monophenol monooxygenase
C:Keywords: oxidoreductase

Query Match 20.1%; Score 57; DB 2; Length 273;
Best Local Similarity 35.9%; Pred. No. 7.8;
Matches 14; Conservative 5; Mismatches 14; Indels 6; Gaps 2;

Qy 7 NFOGLRSFGCRFG---TCTVQKL--AHQIYQFTDKD 39
Db 94 NFMGNCECKFGSGQNCETERLRTRRNIFOLTISEKD 132

RESULT 15
Ti4529
S:locus-specific glycoprotein - wild cabbage (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica oleracea (wild cabbage)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
 C:Accession: T14529
 R:Kusaba M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
 Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
 A:Title: Striking sequence similarity in inter- and intra-specific comparisons of class
 mechanism.
 A:Reference number: Z18078; MUID:97352858
 A:Accession: T14529
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-428 <KUS>
 A:Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142
 C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
 C:Keywords: glycoprotein

Query Match 19.8%; Score 56; DB 2; Length 428;
 Best Local Similarity 31.1%; Pred. No. 17;
 Matches 19; Conservative 9; Mismatches 19; Indels 14; Gaps 3;

QY 6 NNFQGLRS---FCRF-GTCTVOKLAHQIYQFTDKDKD-----NVAPRSKISPOG 51
 Db 207 SGFQVHRSGFWNGVRFSGIPENOKLSIMVINFTEENSEEVAYTFRMTNNSFYSLKRVSSDG 266

QY 52 Y 52
 Db 267 Y 267

Search completed: October 17, 2002, 14:46:18
 Job time : 6.96509 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:21 ; Search time 3.11222 Seconds
(without alignments)
646.939 Million cell updates/sec

Title: US-10-018-924-2_COPY_95_146

Perfect score: 283

Sequence: 1 YRQSMNFGQLRSGCRFGT.....FTDKDKDNVAPRSKISPOGY 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	283	100.0	185	ADML_HUMAN	P35318 homo sapien
2	277	97.9	188	ADML_PIG	P53366 sus scrofa
3	265	93.6	188	ADML_CANFA	O77559 canis famil
4	263	92.9	188	ADML_BOVIN	O62827 bos taurus
5	231	81.6	185	ADML_RAT	P43145 rattus norv
6	222	78.4	184	ADML_MOUSE	P97297 mus musculu
7	65.5	23.1	532	TYRO_RANNI	Q04604 rana nigrom
8	61	21.6	1541	MRP2_RAT	Q63120 rattus norv
9	59	20.8	273	TYRO_COTJA	Q08410 coturnix co
10	59	20.8	1545	MRP2_HUMAN	Q92887 homo sapien
11	57	20.1	529	TYRO_CHICK	P55024 gallus gall
12	55	19.4	425	SVH_METTH	O26346 methanobact
13	55	19.4	1564	MRP2_RABIT	Q28689 oryctolagus
14	54.5	19.3	436	SUS6_BRAOL	P07761 brassica ol
15	53	18.7	529	TYRO_HUMAN	P14679 homo sapien
16	53	18.7	672	KPCA_BOVIN	P04409 bos taurus
17	53	18.7	672	KPCA_HUMAN	P17252 homo sapien
18	53	18.7	672	KPCA_MOUSE	P20444 mus musculu
19	53	18.7	672	KPCA_RABIT	P10102 oryctolagus
20	53	18.7	672	KPCA_RAT	P05696 rattus norv
21	52	18.4	273	TYRO_CANFA	P54834 canis famil
22	52	18.4	439	FGI2_HUMAN	Q14314 homo sapien
23	52	18.4	485	GATA_BACSU	O08491 bacillus su
24	51.5	18.2	305	LIGD_PSEPA	Q01198 pseudomonas
25	51.5	18.2	442	TOP5_BPT4	P07065 bacterioph
26	51.5	18.2	1268	VGLN_HUMAN	Q00341 homo sapien
27	51	18.0	180	VG48_BPMU	O911v1 bacterioph
28	51	18.0	273	TYRO_TRIST	P55026 trionyx sin
29	51	18.0	566	MXID_SHIFL	Q04641 shigella fl
30	51	18.0	566	MXID_SHISO	Q55293 shigella so
31	51	18.0	985	ENV_SEV1	P23073 shman foam
32	51	18.0	1325	MRP4_HUMAN	O15439 homo sapien
33	50.5	17.8	459	G33_RAT	P05432 rattus norv

34	50.5	17.8	805	1	FUSE_DROME	P23647 drosophila
35	50.5	17.8	922	1	YKE0_YEAST	P35736 saccharomyc
36	50	17.7	336	1	D3H1_HUMAN	P31937 homo sapien
37	50	17.7	354	1	I824_HUMAN	P30470 homo sapien
38	50	17.7	362	1	I835_HUMAN	Q947d7 lactococcus
39	50	17.7	399	1	GALI1_IACLA	Q99504 homo sapien
40	50	17.7	573	1	EYA3_HUMAN	P56869 chlamydia m
41	50	17.7	1252	1	RPOB_CHLMU	O929a0 chlamydia p
42	50	17.7	1252	1	RPOB_CHLPN	O84317 chlamydia t
43	50	17.7	1252	1	RPOB_CHLPR	Q62245 mus musculu
44	50	17.7	1319	1	SOS1_MOUSE	Q07889 homo sapien
45	50	17.7	1333	1	SOS1_HUMAN	

ALIGNMENTS

RESULT 1
ID ADML_HUMAN STANDARD; PRT; 185 AA.
AC P35318;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM OR AM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pheochromocytoma;
RX MEDLINE=93343928; PubMed=7688224;
RA Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT "Cloning and characterization of cDNA encoding a precursor for human adrenomedullin.";
RL Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94354869; PubMed=8074714;
RA Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA Kitamura K., Eto T., Matsuo H.;
RT "Genomic structure of human adrenomedullin gene.";
RL Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN [3]
RP SEQUENCE OF 95-146.
RC TISSUE=Pheochromocytoma;
RX MEDLINE=93249425; PubMed=8387282;
RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA Matsuo H., Eto T.;
RT "Adrenomedullin: a novel hypotensive peptide isolated from human pheochromocytoma.";
RL Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN [4]
RP REVIEW.
RX MEDLINE=98240137; PubMed=9578982;
RA Samson W.K.;
RT "Proadrenomedullin-derived peptides.";
RL Front. Neuroendocrinol. 19:100-127(1998).
RN [5]
RP REVIEW.
RX MEDLINE=20053666; PubMed=10588445;
RA Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT "Structure-activity relationships of adrenomedullin in the circulation and adrenal gland.";
RL Regul. Pept. 85:1-8(1999).
CC -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP

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DR EMBL; D15069; BAA03665.1; -;
DR EMBL; U15419; AAB60519.1; -;
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 91 BY SIMILARITY.
FT PEPTIDE 94 143 ADRENOMEDULLIN.
FT PROPEP 149 185 PREPROAM C-TERMINAL FRAGMENT (BY SIMILARITY).
FT DISULFID 107 112 BY SIMILARITY.
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP)
FT SEQUENCE 185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;

Query Match 81.6%; Score 231; DB 1; Length 185;
Best Local Similarity 84.6%; Pred. No. 1.2e-23;
Matches 44; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 YRQSMNFGRLSFCRGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
DB 94 YRQSMN--QGSRTGCRFGCTCTVQKLAHQIYQFTDKDKDGMAPRNKISPOGY 143

RESULT 6

ADML_MOUSE
ID ADML_MOUSE STANDARD; PRT; 184 AA.
AC P97297; P97453;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (PROAM-N20) (PROAM N-terminal 20 peptide) (PAMP)].
GN ADM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97092892; PubMed=938454;
RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RA "Genomic organization, expression, and chromosomal mapping of the rat mouse adrenomedullin gene";
RL Genomics 37:395-399(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Yotsumoto S., Ko M.S.H.;
RA "Expression of mouse adrenomedullin gene in trophoblastic giant cells at the implantation site";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR AGENTS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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DR EMBL; D78349; BAA11367.1; -;
DR MGD; U77630; AAB36535.1; -;
DR MGD; MGI:108058; Adm.
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 92 BY SIMILARITY.
FT PEPTIDE 95 144 ADRENOMEDULLIN.
FT PROPEP 151 184 PREPROAM C-TERMINAL FRAGMENT (BY SIMILARITY).
FT DISULFID 108 113 BY SIMILARITY.
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT MOD_RES 144 144 AMIDATION (G-145 PROVIDE AMIDE GROUP)
FT CONFLICT 173 173 A -> G (IN REF. 2).
SQ SEQUENCE 184 AA; 20764 MW; C88C9045A79C898 CRC64;

Query Match 78.4%; Score 222; DB 1; Length 184;
Best Local Similarity 82.7%; Pred. No. 1.8e-22;
Matches 43; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 YRQSMNFGRLSFCRGCTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
DB 95 YRQSMN--QGSRTGCRFGCTCTVQKLAHQIYQFTDKDKDGMAPRNKISPOGY 144

RESULT 7

TYRO_RANNI
ID TYRO_RANNI STANDARD; PRT; 532 AA.
AC Q04604;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
GN TYR OR TYRS.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077054; PubMed=1446833;
RA Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.;
RA "Cloning and sequencing of the cDNA encoding tyrosinase of the Japanese pond frog, Rana nigromaculata";
RL Gene 121:359-363(1992).
RN [2]
RP SEQUENCE OF 1-277 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95290234; PubMed=7772385;
RA Miura I., Okumoto H., Makino K., Nakata A., Nishioka M.;
RA "Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculata: cloning and nucleotide sequence of the genomic DNA containing the tyrosinase gene and its flanking regions";
RL Jpn. J. Genet. 70:79-82(1995).
CC -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPAQURONE + H(2)O.
CC -1- COFACTOR: BINDS TWO COPPER IONS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.

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EMBL; D12514;	BAA02077.1;	-
EMBL; D37779;	BAA07034.1;	-
P/R; JC1392;	JC1392.	
DR	InterPro; IPR002227;	Tyrosinase.
DR	Pfam; PF00264;	tyrosinase; 1.
DR	PRINTS; PS00092;	TYROSINASE.
DR	PROSITE; PS00497;	TYROSINASE_1; 1.
DR	PROSITE; PS00498;	TYROSINASE_2; 1.
KW	Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;	
KW	Transmembrane; Melanin biosynthesis.	
FT	SIGNAL	1 19 POTENTIAL.
FT	CHAIN	20 532 TYROSINASE.
FT	DOMAIN	20 475 LUMENAL, MELANOSOME (POTENTIAL).
FT	TRANSMEM	476 499 POTENTIAL.
FT	DOMAIN	500 532 CYTOPLASMIC (POTENTIAL).
FT	METAL	184 184 COPPER A (BY SIMILARITY).
FT	METAL	206 206 COPPER A (BY SIMILARITY).
FT	METAL	215 215 COPPER A (BY SIMILARITY).
FT	METAL	367 367 COPPER B (BY SIMILARITY).
FT	METAL	371 371 COPPER B (BY SIMILARITY).
FT	METAL	394 394 COPPER B (BY SIMILARITY).
FT	CARBOHYD	90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	115 115 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	341 341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARIANT	10 T -> A.
SQ	SEQUENCE	532 AA; 60115 MW; B27D3080FC074B3A CRC64:

Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T., Keppeler D.;
"cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance protein, cMRP, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats.";
J. Biol. Chem. 271:15091-15098(1996).
[3]
SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
Ito K., Suzuki H., Hirohashi T., Kume K., Shimizu T., Sugiyama Y.;
"Expression of the putative ATP-binding cassette region, homologous to that in multidrug resistance associated protein (MRP), is hereditarily defective in Eisai hyperbilirubinemic rats (EHRB).";
Int. Hepatol. Commun. 292:292-299(1996).
CC -1- FUNCTION: MEDIATES HEPATOBIILIARY EXCRETION OF NUMEROUS ORGANIC ANIONS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
CC -1- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED HYPERBILIRUBINEMIA (EHRB).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
CC
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CC
CC EMBL; L49379; AAC42087.1; -;
DR DR EMBL; X96393; CAA65257.1; -;
DR DR EMBL; D85086; BAA13016.1; -;
DR DR HSPSP; P13569; INED.
DR DR InterPro; IPR003593; AAA.
DR DR InterPro; IPR001140; ABC_transporter_tmem.
DR DR InterPro; IPR003439; ABC_transporter.
DR DR InterPro; IPR001687; ATP_GTP_A.
DR DR Pfam; PF00664; ABC_membrane; 2.
DR DR Pfam; PF00005; ABC_tran; 2.
DR DR SMART; SM00382; AAA; 1.
DR DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 26 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 27 47 1 (BY SIMILARITY).
FT FT DOMAIN 48 67 CYTOPLASMIC (BY SIMILARITY).
FT FT TRANSMEM 68 88 2 (BY SIMILARITY).
FT FT DOMAIN 89 92 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 93 113 CYTOPLASMIC (BY SIMILARITY).
FT FT DOMAIN 114 125 3 (BY SIMILARITY).
FT FT TRANSMEM 126 145 4 (BY SIMILARITY).
FT FT DOMAIN 147 164 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 165 185 5 (BY SIMILARITY).
FT FT DOMAIN 186 309 CYTOPLASMIC (BY SIMILARITY).
FT FT TRANSMEM 310 330 6 (BY SIMILARITY).
FT FT DOMAIN 331 356 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 357 377 7 (BY SIMILARITY).
FT FT DOMAIN 378 433 CYTOPLASMIC (BY SIMILARITY).
FT FT TRANSMEM 434 454 8 (BY SIMILARITY).
FT FT DOMAIN 455 457 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 458 478 9 (BY SIMILARITY).
FT FT DOMAIN 479 540 CYTOPLASMIC (BY SIMILARITY).
FT FT TRANSMEM 541 561 10 (BY SIMILARITY).
FT FT DOMAIN 562 583 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 584 604 11 (BY SIMILARITY).
FT FT DOMAIN 605 967 CYTOPLASMIC (BY SIMILARITY).
FT FT TRANSMEM 968 988 12 (BY SIMILARITY).
FT FT DOMAIN 989 1029 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 1030 1050 13 (BY SIMILARITY).
FT FT DOMAIN 1051 1093 CYTOPLASMIC (BY SIMILARITY).
FT FT TRANSMEM 1094 1114 14 (BY SIMILARITY).
FT FT DOMAIN 1115 1115 EXTRACELLULAR (BY SIMILARITY).
FT FT TRANSMEM 1116 1136 15 (BY SIMILARITY).
FT FT TRANSMEM 1116 1136

```

FT DOMAIN 1137 1207 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 1208 1228 16 (BY SIMILARITY).
FT DOMAIN 1229 1230 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1231 1251 17 (BY SIMILARITY).
FT DOMAIN 1252 1541 CYTOPLASMIC (BY SIMILARITY).
FT NP_BIND 667 674 ATP (POTENTIAL).
FT NP_BIND 1330 1337 ATP (POTENTIAL).
FT CARBOHYD 1007 1007 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1010 1010 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1011 1011 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 420 420 M -> V (IN REF. 3).
SQ SEQUENCE 1541 AA; 173383 MW; D5PB55571BFDB39 CRC64;

Query Match 21.6%; Score 61; DB 1; Length 1541;
Best Local Similarity 38.2%; Pred. No. 4.8;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQ 51
Db 1479 FSQCTVITIAHRLHTIMDSKIMVLDNGKIVEYG 1512

RESULT 9
ID TYRO_COTJA STANDARD; PRT; 273 AA.
AC Q08410;
DT 01-OCT-1996 (Rel. 34, Created)
DE 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
DE (Fragment).
OS TYR.
GN Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93181407; PubMed=1292011;
RA Yamamoto H., Kudo T., Masuko N., Miura H., Sato S., Tanaka M.,
RA Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;
RT Phylogeny of regulatory regions of vertebrate tyrosinase genes.";
RL Pigment Cell Res. 5:284-294(1992).
CC -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
CC COMPOUNDS, CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
CC DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
CC INDOLE-5,6 QUINONE.
CC -1- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
CC DOPAquinone + H(2)O.
CC -1- COFACTOR: BINDS TWO COPPER IONS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S56788; AAB25510.1; .
CC InterPro: IPR002227; Tyrosinase.
CC Pfam: PF00264; Tyrosinase_1.
CC PROSITE; PS00497; TYROSINASE_1; 1.
CC PROSITE; PS00498; TYROSINASE_2; PARTIAL.
CC Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
CC Transmembrane; Melanin biosynthesis.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 >273 TYROSINASE.

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FT METAL 180 180 COPPER A (BY SIMILARITY).
FT METAL 202 202 COPPER A (BY SIMILARITY).
FT METAL 211 211 COPPER A (BY SIMILARITY).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 273 273
SQ SEQUENCE 273 AA; 31499 MW; 0EA3DE55BE1EA1A CRC64;

Query Match 20.8%; Score 59; DB 1; Length 273;
Best Local Similarity 35.9%; Pred. No. 1.5;
Matches 14; Conservative 6; Mismatches 13; Indels 6; Gaps 2;

Qy 7 NFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD 39
Db 94 NFMGNCGECKFGSGQCTERRLRTRNIFQLTIREKD 132

RESULT 10
MRP2_HUMAN STANDARD; PRT; 1545 AA.
AC Q92887; Q99663; Q92798; Q14022; Q92500; Q9UMS2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Canalicular multispecific organic anion transporter 1 (Multidrug
DE resistance-associated protein 2) (Canalicular multidrug resistance
DE protein).
DE ABC22 OR CMONT1 OR CMONT OR MRP2 OR CMRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96390592; PubMed=8797578;
RA Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M.,
RA Kagotani K., Okumura K., Akiyama S., Kuwano M.;
RT "A human canalicular multispecific organic anion transporter (CMOAT)
RT gene is overexpressed in cisplatin-resistant human cancer cell lines
RT with decreased drug accumulation.";
RL Cancer Res. 56:4124-4129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA KOOL M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,
RA Baas F., Borst P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96279006; PubMed=8662992;
RA Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horle T.,
RA Keppler D.;
RT "cDNA cloning of the hepatocyte canalicular isoform of the multidrug
RT resistance protein, cmrp, reveals a novel conjugate export pump
RT deficient in hyperbilirubinemic mutant rats.";
RL J. Biol. Chem. 271:15091-15098(1996).
RN [4]
RP REVISIONS.
RA Keppler D.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99395001; PubMed=10464142;
RA Tsujii H., Koenig J., Rost D., Stoeckel B., Leuschner U., Keppler D.;
RT "Exon-intron organization of the human multidrug-resistance protein 2
RT (MRP2) gene mutated in Dubin-Johnson syndrome.";
RL Gastroenterology 117:653-660(1999).
RN [6]
RP VARIANT DJS TRP-768.
RX MEDLINE=98087571; PubMed=9425227;
RA Wada M., Toh S., Taniguchi K., Nakamura T., Uchiumi T., Kohno K.,
RA Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;

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"Mutations in the canalicular multispecific organic anion transporter (cMOAT) gene, a novel ABC transporter, in patients with hyperbilirubinemia II/Dubin-Johnson syndrome."; Hum. Mol. Genet. 7:203-207(1998). [7]

VARIANTS DJS TRP-768 AND ARG-1382. MEDLINE-99162196; PubMed-10053008; Toh S., Wada M., Uchiumi T., Inokuchi A., Makino Y., Horie Y., Adachi Y., Sakisaka S., Kuwano M.; "Genomic structure of the canalicular multispecific organic anion-transporter gene (MRP2/cMOAT) and mutations in the ATP-binding-cassette region in Dubin-Johnson syndrome."; Am. J. Hum. Genet. 64:739-746(1999).

-1- FUNCTION: MEDIATES HEPATOBLILIARY EXCRETION OF NUMEROUS ORGANIC ANIONS. MAY FUNCTION AS A CELLULAR CISPLATIN TRANSPORTER. -1- SUBCELLULAR LOCATION: Integral membrane protein. -1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER. -1- DISEASE: DEFECTS IN ABCG2 ARE A CAUSE OF DUBIN-JOHNSON SYNDROME (DJS), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY CONJUGATED HYPERBILIRUBINEMIA, AN INCREASE IN THE URINARY EXCRETION OF COPROPORPHYRIN ISOMER I, DEPOSITION OF MELANIN-LIKE PIGMENT IN HEPATOCYTES, AND PROLONGED RETENTION OF SULFOBROMOPHTHALEIN, BUT OTHERWISE NORMAL LIVER FUNCTION. -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.

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DR EMBL: U63970; AAB39892.1; -
DR EMBL: U49248; AAB09422.1; -
DR EMBL: X96395; CAA6259.2; -
DR EMBL: AJ132244; CAB45309.1; JOINED.
DR EMBL: AJ132287; CAB45309.1; JOINED.
DR EMBL: AJ245625; CAB45309.1; JOINED.
DR EMBL: AJ132286; CAB45309.1; JOINED.
DR EMBL: AJ132289; CAB45309.1; JOINED.
DR EMBL: AJ132290; CAB45309.1; JOINED.
DR EMBL: AJ132291; CAB45309.1; JOINED.
DR EMBL: AJ132292; CAB45309.1; JOINED.
DR EMBL: AJ132293; CAB45309.1; JOINED.
DR EMBL: AJ132294; CAB45309.1; JOINED.
DR EMBL: AJ132295; CAB45309.1; JOINED.
DR EMBL: AJ132296; CAB45309.1; JOINED.
DR EMBL: AJ132297; CAB45309.1; JOINED.
DR EMBL: AJ132298; CAB45309.1; JOINED.
DR EMBL: AJ132299; CAB45309.1; JOINED.
DR EMBL: AJ133000; CAB45309.1; JOINED.
DR EMBL: AJ133001; CAB45309.1; JOINED.
DR EMBL: AJ133002; CAB45309.1; JOINED.
DR EMBL: AJ133003; CAB45309.1; JOINED.
DR EMBL: AJ245626; CAB45309.1; JOINED.
DR EMBL: AJ132304; CAB45309.1; JOINED.
DR EMBL: AJ132305; CAB45309.1; JOINED.
DR EMBL: AJ132306; CAB45309.1; JOINED.
DR EMBL: AJ132307; CAB45309.1; JOINED.
DR EMBL: AJ132308; CAB45309.1; JOINED.
DR EMBL: AJ245627; CAB45309.1; JOINED.
DR EMBL: AJ132309; CAB45309.1; JOINED.
DR EMBL: AJ132310; CAB45309.1; JOINED.
DR EMBL: AJ132311; CAB45309.1; JOINED.
DR EMBL: AJ132312; CAB45309.1; JOINED.
DR EMBL: AJ132313; CAB45309.1; JOINED.
DR EMBL: AJ132314; CAB45309.1; JOINED.
DR HSSP: P13569; 1NBD.
DR MIM: 601107; -
DR MIM: 237500; -
DR InterPro: IPR003593; AAA.
DR InterPro: IPR001140; ABC_transporter_tmem.

DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
KW Disease mutation.
FT DOMAIN 1 27 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 28 48 1 (BY SIMILARITY).
FT DOMAIN 49 68 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 69 89 2 (BY SIMILARITY).
FT DOMAIN 90 93 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 94 114 3 (BY SIMILARITY).
FT DOMAIN 115 126 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 127 147 4 (BY SIMILARITY).
FT DOMAIN 148 165 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 166 186 5 (BY SIMILARITY).
FT DOMAIN 187 313 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 314 334 6 (BY SIMILARITY).
FT DOMAIN 335 360 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 361 381 7 (BY SIMILARITY).
FT DOMAIN 382 437 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 438 458 8 (BY SIMILARITY).
FT DOMAIN 459 461 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 462 482 9 (BY SIMILARITY).
FT DOMAIN 483 544 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 545 565 10 (BY SIMILARITY).
FT DOMAIN 566 587 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 588 608 11 (BY SIMILARITY).
FT DOMAIN 609 971 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 972 992 12 (BY SIMILARITY).
FT DOMAIN 993 1033 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1034 1054 13 (BY SIMILARITY).
FT DOMAIN 1055 1097 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 1098 1118 14 (BY SIMILARITY).
FT DOMAIN 1119 1119 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1120 1140 15 (BY SIMILARITY).
FT DOMAIN 1141 1211 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 1212 1232 16 (BY SIMILARITY).
FT DOMAIN 1233 1234 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1235 1255 17 (BY SIMILARITY).
FT DOMAIN 1256 1545 CYTOPLASMIC (BY SIMILARITY).
FT NP_BIND 671 ATP (POTENTIAL).
FT NP_BIND 1334 1341 ATP (POTENTIAL).
FT CARBOHYD 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1011 1011 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 768 R -> W (IN DJS).
FT VARIANT 1382 /FTIG-VAR_000099.
FT VARIANT 1382 Q -> R (IN DJS).
FT CONFLICT 1188 /FTIG-VAR_010756.
FT CONFLICT 1188 V -> E (IN REF. 2).
FT CONFLICT 1430 V -> G (IN REF. 5).
FT CONFLICT 1515 C -> Y (IN REF. 2).
SQ SEQUENCE 1545 AA; 174190 MW; EA126684DD0F391 CRC64;
Query Match 20.8%; Score 59; DB 1; Length 1545;
Best Local Similarity 37.8%; Pred. No. 8.9;
Matches 14; Conservative 5; Mismatches 14; Indels 4; Gaps 1;
QY 18 FGTCTVQKLAHQIYQFTDKDKONVAPRSKI---SPQ 50
Db 1483 FAHCTVITTAHRLHTIMDSKVMVLDNGKIIEGSP 1519
|||||:||||:|||||
RESULT 11
ID TYRO_CHICK STANDARD; PRT; 529 AA.
AC P55024;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

QY      7 NFOGLRSGCFRGFG---TCTVQKL--AHQIQYQFTDKDKD 39
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      94 NFMFGNCGECKFGFGQNCCTERRLRTRNFQLTISEKD 132

RESULT 12
SYH_METTH
ID   SYH_METTH          STANDARD;          PRT;          425 AA.
AC   O26346;
DT   15-JUL-1998 (Rel. 36, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE   (HISRS).
DE   DE
GN   HISS OR MTH244.
OS   Methanobacterium thermoautotrophicum.
OC   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC   Methanothermobacter.
OX   NCBI_TaxID=145262;
RN   [1]
RS   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE=98037514; PubMed=9371463;
RA   Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA   Adridge T., Bashirzaadeh R., Blakely D., Cook R., Gilbert K.,
RA   Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA   Spadafora R., Vicare R., Wang Y., Wlierzowski J., Gibson R.,
RA   Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA   McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA   Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT   "Complete genome sequence of Methanobacterium thermoautotrophicum
RT   deltaH: functional analysis and comparative genomics.";
RL   J. Bacteriol. 179:7135-7155(1997).
CC   -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
CC   diphosphate + L-histidyl-tRNA(His).
CC   -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
-----
DR   EMBL; AE000811; AB84750.1; ALT_INIT.
DR   HSSP; O32422; 10EO.
DR   InterPro; IPR002106; AA_trna_ligase_II.
DR   InterPro; IPR004154; HGTP_anticonodon.
DR   InterPro; IPR002314; tRNA-synt_2b.
DR   Pfam; PF03129; HGTP_anticonodon; 1.
DR   Pfam; PF00587; tRNA-synt_2b; 1.
DR   PROSITE; PS00179; AA-trNA-LIGASE_II_1; FALSE_NEG.
DR   PROSITE; PS00339; AA-trNA-LIGASE_II_2; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Complete proteome.
SQ   SEQUENCE 425 AA; 48019 MW; 8388A5975A017535 CRC64;

Query Match          19.4%; Score 55; DB 1: Length 425;
Best Local Similarity 31.7%; Pred. NO. 8;
Matches 13; Conservative 11; Mismatches 13; Indels 4; Gaps 1;

QY      8 FQGLRSGCFRGFGTCTVQKLAHQIQYQFTDKDKDNVAPRSKIS 48
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      44 FEELKLFVTKSG---EEVYNQIYHFDKGGRELALRPFLT 80

RESULT 13
MRP2_RABIT
ID   MRP2_RABIT
AC   Q28689;
STANDARD;          PRT;          1564 AA.

```



```

RN [24]
RX VARIANT GLN-402.
RP MEDLINE=97301760; PubMed=9158138;
RA Morell R., Spritz R.A., Ho L., Pierpont J., Guo W., Friedman T.B.,
RA Asher J.H. Jr.;
RT "Apparent digenic inheritance of Waardenburg syndrome type 2 (WS2) and
RL autosomal recessive ocular albinism (AROA).";
RM Hum. Mol. Genet. 6:659-664(1997).
RN [25]
RX VARIANTS OCA-IA AND OCA-IB.
RP MEDLINE=97403941; PubMed=9259202;
RA Spritz R.A., Oh J., Fukai K., Holmes S.A., Ho L., Chitayat D.,
RA France T.D., Musarella M.A., Orlow S.J., Schnur R.E., Weleber R.G.,
RA Levin A.V.;
RT "Novel mutations of the tyrosinase (TYR) gene in type I
RL oculocutaneous albinism (OCA1).";
RM Hum. Mutat. 10:171-174(1997).
RN [26]
RX VARIANTS OCA-IA AND OCA-IB.
RA Oetting W.S., Fryer J.P., King R.A.;

Query Match      18.7%; Score 53; DB 1; Length 529;
Best Local Similarity 30.2%; Pred. No. 19;
Matches 13; Conservative 6; Mismatches 18; Indels 6; Gaps

QY   3 QSMNNFQGLRSFCGRFG----TCTVQKL--AHQIQFTDKDKD 39
    +  |||          ||::||         |::|
DB   90 QCSNPMGFMGCNGKCFGWGPNCPTERRLLVRNRIFDLSPAEPK 132

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 9.48534 Seconds
(without alignments)
742.931 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185

Perfect score: 947

Sequence: 1 VSVALLMGLSLAFLGADTAR.....SKPQAHGAPAPPSGAPHFL 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	% Query	Description
1	947	100.0	185	ADML_HUMAN
2	817	86.3	188	ADML_PIG
3	774.5	81.8	188	ADML_BOVIN
4	771	81.4	188	ADML_CANFA
5	624.5	65.9	185	ADML_RAT
6	570	60.2	184	ADML_MOUSE
7	89.5	9.3	326	TTP_HUMAN
8	89	9.4	224	FA5_HUMAN
9	88.5	9.3	397	CEFD_STRCL
10	87	9.2	450	A2AA_MOUSE
11	87	9.2	656	DNAA_STRCO
12	83.5	8.8	574	MP12_RAT
13	82	8.7	450	A2AA_RAT
14	80.5	8.5	682	TBR1_HUMAN
15	80	8.4	250	REPA_AGRTO
16	80	8.4	458	YNE1_CAEEL
17	79	8.3	320	TTP_RAT
18	79	8.3	450	A2AA_HUMAN
19	78.5	8.3	481	KRI_HSV2H
20	78.5	8.3	589	VP40_SCMVC
21	78.5	8.3	1796	YRF1_YEAST
22	78.5	8.3	2145	CYAA_PODAN
23	78	8.2	519	GAG_SIVAT
24	78	8.2	678	T2D5_MOUSE
25	77.5	8.2	1382	YRF4_YEAST
26	77.5	8.2	1681	YRF2_YEAST
27	77.5	8.2	1859	YRF3_YEAST
28	77.5	8.2	1859	YRF6_YEAST
29	77	8.1	591	PTRR_MOUSE
30	77	8.1	678	T2D5_RAT
31	76.5	8.1	450	A2AA_PIG
32	76.5	8.1	681	TBR1_MOUSE
33	76	8.0	410	ICPO_PRVIF

34	75.5	8.0	2845	1	APC_MOUSE
35	75	7.9	319	1	TTP_MOUSE
36	75	7.9	429	1	ELK1_MOUSE
37	75	7.9	591	1	PTRR_RAT
38	75	7.9	825	1	ICPO_HSV2H
39	75	7.9	1089	1	IMB3_YEAST
40	74.5	7.9	127	1	CAL2_HUMAN
41	74.5	7.9	324	1	TTP_BOVIN
42	74.5	7.9	389	1	CBX8_HUMAN
43	74.5	7.9	933	1	PRGR_HUMAN
44	74	7.8	423	1	BRAC_BRARE
45	74	7.8	2254	1	CCAG_RAT

ALIGNMENTS

RESULT 1
ADML_HUMAN
ID ADML_HUMAN STANDARD; PRT; 185 AA.
AC P35318;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM OR AM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pheochromocytoma;
RX MEDLINE=93343928; PubMed=7688224;
RA Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT "Cloning and characterization of cDNA encoding a precursor for human
RT adrenomedullin.";
RL Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=943544869; PubMed=8074714;
RA Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuo H.,
RA Kitamura K., Eto T., Matsuo H.;
RT "Genomic structure of human adrenomedullin gene.";
RL Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN [3]
RP SEQUENCE OF 95-146.
RC TISSUE=Pheochromocytoma;
RX MEDLINE=93249425; PubMed=8387282;
RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA Matsuo H., Eto T.;
RT "Adrenomedullin: a novel hypotensive peptide isolated from human
RT pheochromocytoma.";
RL Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN [4]
RP REVIEW.
RX MEDLINE=98240137; PubMed=9578982;
RA Samson W.K.;
RT "Proadrenomedullin-derived peptides.";
RL Front. Neuroendocrinol. 19:100-127(1998).
RN [5]
RP REVIEW.
RX MEDLINE=20053666; PubMed=10588445;
RA Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT "Structure-activity relationships of adrenomedullin in the circulation
RT and adrenal gland.";
RL Regul. Pept. 85:1-8(1999).
CC -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
CC AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
CC PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
CC KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP

```
CC INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
CC PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
CC INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
CC AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME.
CC ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
CC VESSELS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHROCHROMOCYTOMA AND
CC ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
CC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D14874; BAA03589.1; -
DR EMBL; S73906; AAC60642.1; -
DR EMBL; D43639; BAA07756.1; ALT_SEQ.
DR PIR; JN0476; JN0476.
DR PIR; JN0684; JN0684.
DR MIM; JC2351; JC2351.
DR MIM; J03275; -
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL; 1 21
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 92 ADRENOMEDULLIN.
FT PEPTIDE 95 146 PREPROAM C-TERMINAL FRAGMENT.
FT PROPEP 148 185 ADRENOMEDULLIN.
FT DISULFID 110 115
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ SEQUENCE 185 AA; 20420 MW; 64C7D2A0B4654DFE CRC64;

Query Match 100.08; Score 947; DB 1; Length 185;
Best Local Similarity 100.08; Pred. No. 7.7e-78;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSVLMYLGSLAFLGADTARLDVASEFRKKWKNWALSRGKRELRLSSSYPTGLADYKAGP 60
DB 4 VSVLMYLGSLAFLGADTARLDVASEFRKKWKNWALSRGKRELRLSSSYPTGLADYKAGP 63
QY 61 AQTILRPQDMKGASRSPEDSPDAARIRVKRYRQSMNNFQGLRSFCRGFTCTVOKLAHQ 120
DB 64 AQTILRPQDMKGASRSPEDSPDAARIRVKRYRQSMNNFQGLRSFCRGFTCTVOKLAHQ 123
QY 121 IYQFTDKDKDNVAPRSKISPOQYGRRRRSLPEAGPRTLVSCKPQAHGAPPPSGSAPH 180
DB 124 IYQFTDKDKDNVAPRSKISPOQYGRRRRSLPEAGPRTLVSCKPQAHGAPPPSGSAPH 183
QY 181 FL 182
DB 184 FL 185

RESULT 2
ADML_PIG STANDARD; PRT; 188 AA.
AC P53366;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM OR AM.
OS Sus scrofa (Pig).
```

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CC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Adrenal medulla;
RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA Kitamura K., Kangawa K., Minamino N., Matsuo H., Eto T.;
RT "Complete amino acid sequence of porcine adrenomedullin and cloning
RT of cDNA encoding its precursor.";
RL FEBS Lett. 338:306-310(1994).
RN [2]
RP SEQUENCE OF 22-41.
RC TISSUE-Adrenal medulla;
RX MEDLINE=94357274; PubMed=8076689;
RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT "Identification and hypotensive activity of proadrenomedullin
RT N-terminal 20 peptide (PAMP).";
RL FEBS Lett. 351:35-37(1994).
CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
CC AGENTS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
CC KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D14875; BAA03590.1; -
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL; 1 21
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 92 ADRENOMEDULLIN.
FT PEPTIDE 95 146 PREPROAM C-TERMINAL FRAGMENT (BY
FT PROPEP 153 188 SIMILARITY).
FT DISULFID 110 115 BY SIMILARITY.
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
SQ SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;

Query Match 86.3%; Score 817; DB 1; Length 188;
Best Local Similarity 89.1%; Pred. No. 3.2e-66;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSVLMYLGSLAFLGADTARLDVASEFRKKWKNWALSRGKRELRLSSSYPTGLADYKAGP 60
DB 4 VSVLMYLGSLAFLGADTARLDVASEFRKKWKNWALSRGKRELRLSSSYPTGLADYKAGP 63
QY 61 AQTILRPQDMKGASRSPEDSPDAARIRVKRYRQSMNNFQGLRSFCRGFTCTVOKLAHQ 120
DB 64 AQTILRPQDMKGASRSPEDSPDAARIRVKRYRQSMNNFQGLRSFCRGFTCTVOKLAHQ 123
QY 121 IYQFTDKDKDNVAPRSKISPOQYGRRRRSLPEAGPRTLVSCKPQAHGAPPPS 175
DB 124 IYQFTDKDKDNVAPRSKISPOQYGRRRRSLPEAGPRTLVSCKPQAHGAPPPS 178

RESULT 3
ADML_BOVIN STANDARD; PRT; 188 AA.
ID ADML_BOVIN
AC O62827;
DT 16-OCT-2001 (Rel. 40, Created)
```



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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98244567; PubMed=9585168;
RA Barker S., Wood E., Clark A.J.L., Corder R.;
RT "Cloning of bovine preadrenomedullin and inhibition of its basal
RT expression in vascular endothelial cells by staurosporine.";
RL Life Sci. 62:1407-1415(1998).
CC
CC -!- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CC CIRCULATION CONTROL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC
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CC
DR EMBL; AJ001613; CAA04866.1; -
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PEPTIDE 22 41
FT PROPEP 45 92
FT PEPTIDE 95 146
FT PROPEP 148 188
FT
FT DISULFID 110 115
FT MOD_RES 41 41
FT MOD_RES 146 146
FT MOD_RES 146 146
FT SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;
Query Match 81.8%; Score 774.5; DB 1; Length 188;
Best Local Similarity 87.8%; Pred. No. 2e-62;
Matches 151; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
QY 1 VSVALLMGLSLAFLGADTARLDVASEFRKKNWALSRGKRELRMSSSYPTGLADVKAGP 60
DB 4 VPVALLMGLSLAFLGADTARLDVAAEFRRKKNWALSRGKRELRESSTPTGLADVKAGP 63
QY 61 AQTLLRPQDMKASRSPDPAARIRVKYRQSMNMFQGLRSFGCGFGTCTVOKLAHQ 120
DB 64 VQTLRLPQDMKASRSPQASPDPAARIRVKYRQSLNMFQGLRSFGCGFGTCTVOKLAHQ 123
QY 121 IYQFTDKDKNDVAPRSKISPOGYGRRRRSLPEAGPGRTLVS-SKPOAHGAP 171
DB 124 IYHFTDKDKDGSAPRSKISPOGYGRRRRSLPEAGLGRTLTLPPEPKLRGAP 175
RESULT 4
ID ADM_CANFA STANDARD; PRT; 188 AA.
AC 077559; Q9TVG9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20

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DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Imoto I., Jougasaki M.;
RT "Cloning of cDNA encoding canine adrenomedullin.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99002704; PubMed=9788655;
RA Ono Y., Kojima M., Okada K., Kangawa K.;
RT "cDNA cloning of canine adrenomedullin and its gene expression in the
RT heart and blood vessels in endotoxin shock.";
RL Shock 10:243-247(1998).
CC
CC -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
CC AGENTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC
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CC
DR EMBL; AF045773; AAD05423.1; -
DR EMBL; U96127; AAD09957.1; -
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PEPTIDE 22 41
FT PROPEP 45 92
FT PEPTIDE 95 146
FT PROPEP 148 188
FT
FT DISULFID 110 115
FT MOD_RES 41 41
FT MOD_RES 146 146
FT MOD_RES 146 146
FT CONFLICT 130 130
FT SEQUENCE 188 AA; 20929 MW; 809D6A64F98F5578 CRC64;
Query Match 81.4%; Score 771; DB 1; Length 188;
Best Local Similarity 86.1%; Pred. No. 4.2e-62;
Matches 149; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 1 VSVALLMGLSLAFLGADTARLDVASEFRKKNWALSRGKRELRMSSSYPTGLADVKAGP 60
DB 4 VPVALLMGLSLAFLGADTARLDVASEFRKKNWALSRGKRELRSSTPTGLAEVKAGP 63
QY 61 AQTLLRPQDMKASRSPDPAARIRVKYRQSMNMFQGLRSFGCGFGTCTVOKLAHQ 120
DB 64 AQTLLRTQDVKGASRNPTSGDPAARIRVKYRQSMNMFQGLRSFGCGFGTCTVOKLAHQ 123
QY 121 IYQFTDKDKNDVAPRSKISPOGYGRRRRSLPEAGPGRTLVS-SKPOAHGAP 173
DB 124 IYQFTDNDKDGVPAPRSKISPOGYGRRRRSLPEPGLRRLTLFPPEPRGGAP 176
RESULT 5
ID ADML_RAT
AC P43145;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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Qy	61	AOTLIRPDMKGASRSPEDSSPDAAIRVKRYQSMNFGLSFGCRGCTCTVQKLAHQ	120
		: : : : :	
Db	64	TOTL-GLOCKOSTSPQASTOSTAIRVKRYQSMN--QGSFSTGCRGCTCTMOKLAHQ	120

Db 4 VSTITLMLGSLAFLGADTAGDPDPSPQFRKKWKNKALSRRKRELQASSSYPTGLADETTVP 63
 QY 61 AQTLLRPQDMKGRASPEDESSPDAAIRIVKRYROSNNFQGLRSGFCRGTCVTKLAHQ 120
 Db 64 TQTLDPFLDEQNTTGLQASNGSEAHIRVKRYRQSMN--QGSNSRCRGTCCTCFKLAHQ 121
 QY 121 IYQFTDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPOAHGAPAP 173
 Db 122 IYQLTDXDKDGMAPRNKISPOGYGRRRRSLLEVLRSRTVSESSQEQTHAPAP 174

RESULT 7

ID TTP_HUMAN STANDARD; PRT; 326 AA.
 AC P2651;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Tristetrapoline (TTP) (TIS11A protein) (TIS11) (ZFP-36) (Growth
 DE factor-inducible nuclear protein NDP475) (GO/G1 switch regulatory
 DE protein 24).
 GN ZFP36 OR TIS11A OR TTP OR GOS24.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91288233; PubMed=2062660;
 RA Taylor G.A., Lai W.S., Oakley R.J., Seldin M.F., Shows T.B.,
 RA Eddy R.L. Jr., Blackshear P.J.;
 RT "The human TTP protein: sequence, alignment with related proteins,
 RT and chromosomal localization of the mouse and human genes.";
 RL Nucleic Acids Res. 19:3454-3454(1991).
 CC -!- FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
 CC STRUCTURE INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.
 CC HAS BEEN EXPERIMENTALLY SHOWN TO BE ABLE TO BIND ZINC.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.
 CC -!- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.

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CC EMBL; M92843; AAA58489.1; -
 DR EMBL; M92844; AAC37600.1; -
 DR EMBL; M63625; AAA61240.1; -
 DR PIR; S34427; S34427.
 DR MIM; 190700; -
 DR InterPro; IPR000571; Zf-CCCH.
 DR Pfam; PF00642; zf-CCCH; 2.
 DR SMART; SM00356; Znf_C3H1; 2.
 KW Nuclear protein; Repeat; Metal-binding; Zinc-finger; DNA-binding.
 FT REPEAT 71 75 P-P-P-P-G.
 FT REPEAT 198 202 P-P-P-P-G.
 FT REPEAT 219 223 P-P-P-P-G.
 FT ZN_FING 109 128 C3H1-TYPE 1.
 FT ZN_FING 147 166 C3H1-TYPE 2.
 SQ SEQUENCE 326 AA; 34003 MW; DDD9AD950AF7AF98 CRC64;

Query Match 9.5%; Score 89.5; DB 1; Length 326;
 Best Local Similarity 22.4%; Pred. No. 0.61;
 Matches 45; Conservative 18; Mismatches 77; Indels 61; Gaps 8;

QY 34 WALSRGKRELNRSSSYPTGLADYKAGPAOTLIRPOD-----MKGASRSPE 78
 Db 32 WGSFGWLSLSPSDSSPSGVTSLRPGRTSLVEGRSCGWPPPPGPAFLAPLRLGPELSPS 90

QY 79 DSSPDAAIRIVKRYROSNNFQGLRSGFCRGTCV-----CRFGT-CTV-----OK 116
 Db 91 PTPSTATSTPTSPRYKTEL-----CRTFSSGRCRYGAKQCFAGHGLGELRQANRHPKYKTE 145
 QY 117 LAHQIYQ-----FTDKDNVAP-----RSKISPOGYGRRRRSLPEAGPGR 158
 Db 146 LCHKFYLOGRCVPYGRCHFIHNPSEDLAAPHPPVLRQISFSFSLSGLSGRTSPFPPLAG 205
 QY 159 TLVSSKPOAHGAPAPPSGAP 179
 Db 206 PSLSSSSFSFSSPPPPGDL 226

RESULT 8

FA5_HUMAN
 ID FA5_HUMAN STANDARD; PRT; 2224 AA.
 AC P12259; Q14285;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coagulation factor V precursor (Activated protein C cofactor).
 GN F5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92232668; PubMed=1567832;
 RA Cripe L.D., Moore K.D., Kane W.H.;
 RT "Structure of the gene for human coagulation factor V.";
 RL Biochemistry 31:3777-3785(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87260886; PubMed=3110773;
 RA Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A.,
 RA Hewick R.M., Kaufman R.J., Mann K.G.;
 RT "Complete cDNA and derived amino acid sequence of human factor V.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
 RN [3]
 RN SEQUENCE OF 1-1600 FROM N.A.
 RX MEDLINE=88107560; PubMed=2827731;
 RA Kane W.H., Ichinose A., Hagen F.S., Davie E.W.;
 RT "Cloning of cDNAs coding for the heavy chain region and connecting
 RT region of human factor V, a blood coagulation factor with four types
 RT of internal repeats.";
 RL Biochemistry 26:6508-6514(1987).
 RN [4]
 RN SEQUENCE OF 1188-1215 AND 1315-2224 FROM N.A.
 RX MEDLINE=86313665; PubMed=3092220;
 RA Kane W.H., Davie E.W.;
 RT "Cloning of a cDNA coding for human factor V, a blood coagulation
 RT factor homologous to factor VIII and ceruloplasmin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
 RN [5]
 RN PARTIAL SEQUENCE FROM N.A.
 RX TISSUE=Fibroblast;
 RC MEDLINE=93203619; PubMed=8454869;
 RA Shen N.L.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
 RA Edgington T.S.;
 RT "The serine protease cofactor factor V is synthesized by
 RT lymphocytes.";
 RL J. Immunol. 150:2992-3001(1993).
 RN [6]
 RN SULFATION.
 RX MEDLINE=94264012; PubMed=8204629;
 RA Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
 RA Kaufman R.J.;
 RT "Posttranslational sulfation of factor V is required for efficient
 RT thrombin cleavage and activation and for full procoagulant activity.";
 RL Biochemistry 33:6952-6959(1994).
 RN [7]

RP SULFATION
RX MEDLINE-90366699; PubMed-2168225;
RA Hortin G.L.;
RT "Sulfation of tyrosine residues in coagulation factor V.";
RL Blood 76:946-952(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 2065-2224.
RX MEDLINE-20052169; PubMed-10586886;
RA Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
Fuentes-Prior P.;
RT "Crystal structures of the membrane-binding C2 domain of human
coagulation factor V";
RL Nature 402:434-439(1999).
RN [9]
RP VARIANT APCR GLN-534.
RX MEDLINE-94217810; PubMed-8164741;
RA Bertina R.J., Koelenen B.P.C., Koster T., Rosendaal F.R.,
Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
RT "Mutation in blood coagulation factor V associated with resistance to
activated protein C";
RL Nature 363:64-67(1994).
RN [10]
CC -!- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
CC -!- SUBUNIT: Factor Va is composed of a heavy chain and a light
chain, noncovalently bound. The interaction between the two chains
is calcium-dependent.
CC -!- DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA
REPEATS.
CC -!- PTM: Thrombin activates factor V proteolytically to the active
cofactor, factor Va (formation of a heavy chain at the N-
terminus and a light chain at the C-terminus).
CC -!- PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND
ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.
CC -!- DISEASE: OMEN PARAHOMOPHILIA, AN HEMORRHAGIC DIATHESIS, IS DUE
TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN F5 RESULTS IN A
FORM OF THROMBOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR
MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT
A SLIGHT THROMBOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
IMPLANTATION.
CC -!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF
2 PLASTOCYANIN-LIKE REPEATS.
CC -!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.

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DR EMBL; L32779; AAB59401.1; JOINED.
DR EMBL; L32755; AAB59401.1; JOINED.
DR EMBL; L32756; AAB59401.1; JOINED.
DR EMBL; L32757; AAB59401.1; JOINED.
DR EMBL; L32758; AAB59401.1; JOINED.
DR EMBL; L32759; AAB59401.1; JOINED.
DR EMBL; L32760; AAB59401.1; JOINED.
DR EMBL; L32761; AAB59401.1; JOINED.
DR EMBL; L32762; AAB59401.1; JOINED.
DR EMBL; L32763; AAB59401.1; JOINED.
DR EMBL; L32764; AAB59401.1; JOINED.
DR EMBL; L32765; AAB59401.1; JOINED.
DR EMBL; L32766; AAB59401.1; JOINED.
DR EMBL; L32767; AAB59401.1; JOINED.
DR EMBL; L32768; AAB59401.1; JOINED.
DR EMBL; L32769; AAB59401.1; JOINED.
DR EMBL; L32770; AAB59401.1; JOINED.
DR EMBL; L32771; AAB59401.1; JOINED.
DR EMBL; L32772; AAB59401.1; JOINED.
DR EMBL; L32773; AAB59401.1; JOINED.

DR EMBL; L32774; AAB59401.1; JOINED.
DR EMBL; L32775; AAB59401.1; JOINED.
DR EMBL; L32776; AAB59401.1; JOINED.
DR EMBL; L32777; AAB59401.1; JOINED.
DR EMBL; L32778; AAB59401.1; JOINED.
DR EMBL; M16967; AAB52424.1; -
DR EMBL; M14335; AAB59532.1; -
DR PIR; A25897; A25897.
DR PIR; A28028; A28028.
DR PDB; 1C2S; 26-NOV-99.
DR PDB; 1C2T; 26-NOV-99.
DR PDB; 1C2V; 26-NOV-99.
DR MIM; 134400; -
DR MIM; 188055; -
DR MIM; 227310; -
DR MIM; 227400; -
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR000421; FA58.C.
DR Pfam; PF00394; Cu-oxidase; 3.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR SMART; SM00231; FA58C; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS01285; FA58C.1; 2.
DR PROSITE; PS01286; FA58C.2; 2.
KW Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
KW Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 2224 COAGULATION FACTOR V.
FT CHAIN 29 737 HEAVY CHAIN.
FT PEPTIDE 738 1573 ACTIVATION PEPTIDE (CONNECTING REGION).
FT CHAIN 1574 2224 LIGHT CHAIN.
FT DOMAIN 30 329 F5/8 TYPE A 1.
FT DOMAIN 203 329 PLASTOCYANIN-LIKE 1.
FT DOMAIN 348 684 F5/8 TYPE A 2.
FT DOMAIN 348 526 PLASTOCYANIN-LIKE 3.
FT DOMAIN 536 684 PLASTOCYANIN-LIKE 4.
FT DOMAIN 692 1573 B.
FT DOMAIN 895 928 2 X 17 AA TANDEM REPEATS.
FT REPEAT 895 911 1-1.
FT REPEAT 912 928 1-2.
FT SIMILAR 1135 1148
FT DOMAIN 1185 1501
FT REPEAT 1185 1193
FT REPEAT 1194 1202 2-1.
FT REPEAT 1203 1211 2-2.
FT REPEAT 1212 1220 2-3.
FT REPEAT 1221 1229 2-4.
FT REPEAT 1230 1238 2-5.
FT REPEAT 1239 1247 2-6.
FT REPEAT 1248 1256 2-7.
FT REPEAT 1257 1265 2-8.
FT REPEAT 1266 1274 2-9.
FT REPEAT 1275 1283 2-10.
FT REPEAT 1284 1292 2-11.
FT REPEAT 1293 1301 2-12.
FT REPEAT 1302 1310 2-13.
FT REPEAT 1311 1319 2-14.
FT REPEAT 1320 1328 2-15.
FT REPEAT 1329 1337 2-16.
FT REPEAT 1338 1346 2-17.
FT REPEAT 1347 1355 2-18.
FT REPEAT 1356 1364 2-19.
FT REPEAT 1365 1373 2-20.
FT REPEAT 1374 1382 2-21.
FT REPEAT 1383 1391 2-22.
FT REPEAT 1392 1400 2-23.
FT REPEAT 1401 1409 2-24.
FT REPEAT 1410 1418 2-25.
FT REPEAT 1419 2-26.

Query Match 9.48; Score 89; DB 1; Length 2224;
Best Local Similarity 23.2%; Pred. No. 6;

Matches	39;	Conservative	26;	Mismatches	71;	Indels	32;	Gaps	5;
QY	3	VALMYLGSIAFLGADTAR-----LDVASEFRKKWKNKWLARGKRELRMSSSYPTGLAD	55						
Db	847	IRLLSLGAEKFSQEHAKHAKPKVERDQAQAKHFRSWMKLLAHKVGRLSQDTGSPSGMRP	906						
QY	56	VKAGPAQTLIRPDMKAGSPED-----SSPDARTIRVRYRQSMNFGQLRSFGCRFT	111						
Db	907	WEDLPQDTPGSPMRPDKPPSLLLLKQSNSTLGVGRHLAS-----	951						
QY	112	CTVOKLAHQIYQTDKDKONVAPRSKISPOGGRRRRRSLPEAG-PGR	158						
Db	952	---EKGSTIEIIQ--DIIDETAVNNWLISPNASRAWGESTPLANKPK	994						
RESULT 9									
ID	CEFD_STRCL	STANDARD;	PRT;	397	AA.				
AC	P18549;								
DT	01-NOV-1990 (Rel. 16, Created)								
DT	01-FEB-1991 (Rel. 17, Last sequence update)								
DT	01-JUN-1994 (Rel. 29, Last annotation update)								
DE	Isopenicillin N epimerase (EC 5.-.-.-)								
GN	CEFD.								
OS	Streptomyces clavuligerus.								
OC	Bacteria; Firmicutes; Actinobacteridae; Actinobacteridae;								
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.								
OX	NCBI_TaxID=1901;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;								
RX	MEDLINE=90299822; PubMed=1694525;								
RA	Kovacevic S., Tobin M.B., Miller J.R.;								
RT	"The beta-lactam biosynthesis genes for isopenicillin N epimerase and								
RT	deacetoxycephalosporin C synthetase are expressed from a single								
RT	transcript in Streptomyces clavuligerus.";								
RL	J. Bacteriol. 172:3952-3958(1990).								
RN	[2]								
RP	SEQUENCE OF 1-23.								
RX	MEDLINE=90028393; PubMed=2804141;								
RA	Usui S., Yu C.-A.;								
RT	"Purification and properties of isopenicillin N epimerase from								
RT	Streptomyces clavuligerus.";								
RL	Biochim. Biophys. Acta 999:78-85(1989).								
CC	-1- FUNCTION: CATALYZES THE REVERSIBLE ISOMERIZATION BETWEEN								
CC	ISOPENICILLIN N AND PENICILLIN N.								
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE.								
CC	-1- PATHWAY: BIOSYNTHESIS OF CEPHALOSPORIN ANTIBIOTICS.								
CC	-1- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT								
CC	AMINOTRANSFERASES.								
CC	-----								
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CC	-----								
DR	EMBL; M32324; AAA26714.1; -.								
DR	InterPro; IPR000192; AminoTransf_class_V.								
DR	pfam; PF00266; aminotran_5; 1.								
DR	PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.								
KW	Antibiotic biosynthesis; isomerase; Pyridoxal phosphate.								
FT	INIT_MET 0								
FT	BINDING 216 216 PYRIDOXAL PHOSPHATE (BY SIMILARITY).								
SQ	SEQUENCE 397 AA; 43366 MW; A152741899F192FF CRC64;								
Query Match									
Best Local Similarity	9.3%; Score 88.5; DB 1; Length 397;								
Matches	46; Conservative 20; Mismatches 63; Indels 57; Gaps 11;								
QY	13	FLGADTARLDVASEFRKKWKNKWLARGKRELRMSSSYPTGLADVKGAPQAQ-TLIRPQDMK	71						

Db	197	FLDLDLSRIP-CDYFAGSGHWWLA-----PTGVGFLHLAGRLELEPTQVS	243						
QY	72	GASRSPEDSPDAARIRVKRYRQSMNFGQLRSFGCRFT-----CTVOKLAHQIYQF	124						
Db	244	WAYEPPEGSGPPAARDR-----FGSTPGLRLECE-GTRDICFWLATPESIDFQ----	291						
QY	125	TDKDKDNVAPRSKISPOGGRRRRRSLPEAG-----PGRTLVS-SKPOAHGAPA----	172						
Db	292	-----AELGP-GAIRARRELTHARRLLADRPGRITLLTPDSPELSGGMVAYRL	339						
QY	173	PPSGSA 178							
Db	340	PGGTD 345							
RESULT 10									
ID	A2AA_MOUSE	STANDARD;	PRT;	450	AA.				
AC	Q01338;								
DT	01-APR-1993 (Rel. 25, Created)								
DT	01-APR-1993 (Rel. 25, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).								
GN	ADRA2A.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=92342131; PubMed=1353249;								
RA	Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;								
RT	"Cloning of two mouse genes encoding alpha 2-adrenergic receptor								
RT	subtypes and identification of a single amino acid in the mouse alpha								
RT	2-C10 homolog responsible for an interspecies variation in								
RT	antagonist binding.";								
RL	Mol. Pharmacol. 42:16-27(1992).								
CC	-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-								
CC	INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G								
CC	PROTEINS.								
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.								
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.								
CC	-----								
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CC	-----								
CC	EMBL; M99377; AAA37213.1; -.								
DR	HSSP; P29274; 1MMH.								
DR	GCRDB; GCR_0439; -.								
DR	MGI; MGI:87934; Adra2a.								
DR	InterPro; IPR000276; GPCR_Rhodpsn.								
DR	pfam; PF00001; 7tm.1; 1.								
DR	PRINTS; PR00237; GPCR_RHODPSN.								
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.								
DR	PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.								
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.								
KW	Multiogene family; Phosphorylation; Lipoprotein; Palmitate.								
FT	DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).								
FT	DOMAIN 34 59 1 (POTENTIAL).								
FT	TRANSMEM 60 70 CYTOPLASMIC (POTENTIAL).								
FT	DOMAIN 71 96 2 (POTENTIAL).								
FT	DOMAIN 97 106 EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM 107 129 3 (POTENTIAL).								
FT	DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).								
FT	TRANSMEM 150 173 4 (POTENTIAL).								
FT	DOMAIN 174 192 EXTRACELLULAR (POTENTIAL).								
FT	TRANSMEM 193 217 5 (POTENTIAL).								


```
RESULT 14
TBR1_HUMAN STANDARD; PRT; 682 AA.
AC Q16650; 1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T-brain-1 protein (T-box brain protein 1) (TBR-1) (TES-56).
GN TBR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95344783; PubMed=7619531;
RA Bulfone A., Smiga S.M., Shimamura K., Peterson A., Puelles L.,
RA Rubenstein J.L.R.;
RT "T-brain-1: a homolog of Brachyury whose expression defines
RT molecularly distinct domains within the cerebral cortex.";
RL Neuron 15:63-78(1995)
CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
CC DEVELOPMENTAL PROCESSES. TBR1 IS REQUIRED FOR NORMAL BRAIN
CC DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear (potential).
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
CC -----
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CC -----
DR EMBL; U49250; AA92010.1; -.
DR HSSP; P24781; 1XBR.
DR MIM; 604616; -.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01264; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
KW DNA_BIND 213 393
FT DOMAIN 569 573 T-BOX.
FT POLY-ALA.
SQ SEQUENCE 682 AA; 74053 MW; E1C8D84206EFBB5 CRC64;

Query Match 8.5%; Score 80.5; DB 1; Length 682;
Best Local Similarity 23.9%; Pred. No. 9;
Matches 34; Conservative 18; Mismatches 59; Indels 31; Gaps 4;

QY 40 KRELHMSSTYPTGLADVKAGPAQTILRPQDMKGASRPEDSSPDAAIRIVKRYQSMNMF 99
| : ||||| : : : : : ||||| : : : : :
Db 15 KKFLNVSSSY-----HSGGSELVLHDHPITSTTNLERSSP-----LKKITRGMTNQ 62

QY 100 QGLRSFGCRFGTCTVQKLAHQIYQFTDKDKNVAPRSKISPOGYG-RRRRSLPEAGPGR 158
| : || ||||| || ||||| || ||||| || |||||
Db 63 SOTDNFP-----DSKDSPGVQRKSLSPVLDGVSELRLHSPFDGSAADR 104

QY 159 TLVSSKPKQAHGAPPPSGAPH 180
| : | | | | | | | | | | | | | | |
Db 105 YLLSQSSQPQSAATAPSAMFPY 126

RESULT 15
REPA_AGRU STANDARD; PRT; 250 AA.
PI5394; 1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Replicating protein.
GN REPA.
OS Agrobacterium tumefaciens.
OG Plasmid pTAR.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88257036; PubMed=3290199;
RA Gallie D.R., Kado C.I.;
RT "Minimal region necessary for autonomous replication of pTAR.";
RL J. Bacteriol. 170:3170-3176(1988).
CC -!- FUNCTION: REQUIRED FOR REPLICATION. IT LIKELY REGULATES PTAR
CC COPY NUMBER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M21299; AAD15307.1; -.
DR PIR; A43662; A43662.
KW Plasmid; DNA replication.
SQ SEQUENCE 250 AA; 27987 MW; CCED106534831979 CRC64;

Query Match 8.4%; Score 80; DB 1; Length 250;
Best Local Similarity 27.2%; Pred. No. 3.2;
Matches 52; Conservative 24; Mismatches 65; Indels 50; Gaps 12;

QY 5 LMYLGLSLFLGADTARLDVA-SEFRKKWNKWLSSRGKRELRLMSSSY-----PTGLAD 55
| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 LDYLTNLVDFG--NGRLDPSISTIMEK-----IGRAESCHSALYPNQRGRPPAGAAD 125

QY 56 VKAGPAQTL-IRPQDMKG-----ASRPEDSSPDAAIR-----VKRYQSMNMFQGLR 103
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 126 KQRLPLEPAGARPRALLGKYVRKAAPLPD-----DAAQAQRERHDTIKAHMDSLSPADRLR 181

QY 104 SFGCRFGTCTVQKLAHQIYQFTDKDKNVAPRSKISPOGYGRRRRRS-----LPAGPGR 158
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 182 E-----TVEDTRAEQLAGYVER-----AAQNRPSGPKAARRROOSRCFTTPNR-PRR 230

QY 159 TLVSSKPKQAHG 169
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 TLPSSHPQKFG 241

Search completed: October 17, 2002, 15:21:38
Job time : 11.4853 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:13 ; Search time 17.1922 Seconds
(without alignments)
1017.222 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185

Perfect score: 947

Sequence: 1 VSVALLYLGLSLAFLGADTAR.....SKPQAHGAPAPSGAPHFEL 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	185	2 JN0684	adrenomedullin pre
2	817	86.3	188	2 S41600	adrenomedullin - p
3	624.5	65.9	185	2 JN0766	adrenomedullin pre
4	95.5	10.1	116	2 T16112	hypothetical prote
5	89.5	9.5	326	2 S34427	tristetraprolin p
6	89	9.4	2224	1 KFHU5	coagulation factor
7	88.5	9.3	398	2 T52311	isopenicillin N ep
8	87	9.2	450	2 I49481	alpha-2 adrenergic
9	87	9.2	656	2 A41870	hypothetical prote
10	83.5	8.8	560	2 T29586	dnaA protein - Str
11	83.5	8.8	574	2 I66868	cdc25B - rat
12	83	8.8	1051	2 C95367	conserved hypothet
13	82.5	8.7	450	2 JH0190	alpha-2-adrenergic
14	81.5	8.6	926	2 F88632	protein F56B3.4 [i
15	81	8.6	450	2 B40392	alpha-2-adrenergic
16	80	8.4	250	2 A43662	replicating protei
17	80	8.4	458	2 S24457	hypothetical prote
18	80	8.4	749	2 I37356	epithelial microtu
19	79	8.3	320	2 JC1255	TIS11 protein - ra
20	79	8.3	383	2 T39597	probable inositol
21	79	8.3	450	2 A34169	alpha-2a-adrenergi
22	78.5	8.3	481	1 B43674	protein kinase (EC
23	78.5	8.3	1196	2 T14108	SH3-containing pro
24	78.5	8.3	1224	2 S28368	hypothetical prote
25	78.5	8.3	1796	2 S65004	probable membrane
26	78.5	8.3	2145	2 JC4747	adenylate cyclase
27	78	8.2	519	1 FOLJG4	gag polyprotein -
28	78	8.2	678	2 JC4245	transcription fact
29	77.5	8.2	199	2 T36622	hypothetical prote

30	77.5	8.2	553	2 T27245	hypothetical prote
31	77.5	8.2	568	2 H88904	protein Y57G1IC.9
32	77.5	8.2	659	2 T27246	hypothetical prote
33	77.5	8.2	723	2 AC1241	polynucleotide pho
34	77.5	8.2	1382	2 S70310	hypothetical prote
35	77.5	8.2	1681	2 S59693	hypothetical prote
36	77.5	8.2	1859	2 S63325	probable membrane
37	77.5	8.2	1859	2 S64633	probable membrane
38	77	8.1	591	2 S44203	parathyroid hormon
39	77	8.1	860	2 T35971	conserved hypothet
40	76.5	8.1	294	2 E88640	protein F55A8.1 [i
41	76.5	8.1	327	2 T02286	hypothetical prote
42	76.5	8.1	450	2 A38316	alpha-2-adrenergic
43	76.5	8.1	581	2 I78558	hypothetical brach
44	76.5	8.1	2374	2 T21052	hypothetical prote
45	76	8.0	327	2 AG3448	transcription regu

ALIGNMENTS

RESULT 1

JN0684
adrenomedullin precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C:Accession: JC2351; JN0684; PN0548; JN0476
R:Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, K.; Kitamura, K.; Eto, T.
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A:Title: Genomic structure of human adrenomedullin gene.
A:Reference number: JC2351; MUID:94354869
A:Accession: JC2351
A:Molecule type: DNA
A:Residues: 1-185 <ISH>
A:Cross-references: GB:S73906; NID:g765329; PIDN:AAC0642.1; PID:g765330
R:Experimental source: pheochromocytoma
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A:Reference number: JN0684; MUID:93343928
A:Accession: JN0684
A:Molecule type: mRNA
A:Residues: 1-185 <KIT>
A:Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A:Accession: PN0548
A:Molecule type: protein
A:Residues: 22-41 <KI2>
R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A:Reference number: JN0476; MUID:93249425
A:Accession: JN0476
A:Molecule type: protein
A:Residues: 95-146 <KI3>
A:Experimental source: pheochromocytoma
C:Genetics:
A:Gene: GDB:ADM
A:Cross-references: GDB:217070; OMIM:103275
A:Map position: llpter-llqter
A:Introns: 33/2; 83/2
C:Keywords: amidated carboxyl end; blood pressure control; hormone
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide
F:95-146/Product: adrenomedullin #status experimental <MAT>
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:147/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:110-115/Disulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following
Query Match 100.0%; Score 947; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 5,2e-80;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  VVALMYLGLSLAFGLGADTARLDVASFRKKWNKWLRSRGRKRELRMSSTPTGLADVKGAP  60
Db      4  VVALMYLGLSLAFGLGADTARLDVASFRKKWNKWLRSRGRKRELRMSSTPTGLADVKGAP  63
QY      61  AQTLLRPQDMKMGASRPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLHAQ  120
Db      64  AQTLLRPQDMKMGASRPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLHAQ  123
QY      121  IYQFTDKDKNVAPRSKISPOGYGRRRRRSLPEAGPGRTLVSSKFPQAHGAPAPPSGSGAPH  180
Db      124  IYQFTDKDKNVAPRSKISPOGYGRRRRRSLPEAGPGRTLVSSKFPQAHGAPAPPSGSGAPH  183
QY      181  FL 182
Db      184  FL 185

RESULT 2
S41600
adrenomedullin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S41600
R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A:Title: Complete amino acid sequence of porcine adrenomedullin and cloning
A:Reference number: S41600; MUID:94139945
A:Accession: S41600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-188 <KIT>
A:Cross-references: GB:D14875; NID:q439721; PIDN:BAA03590.1; PID:g496379

Query Match      86.3%; Score 817; DB 2; Length 188;
Best Local Similarity 89.1%; Pred. No. 5.1e-68;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps

QY      1  VVALMYLGLSLAFGLGADTARLDVASFRKKWNKWLRSRGRKRELRMSSTPTGLADVKGAP  60
Db      4  VVALMYLGLSLAFGLGADTARLDVASFRKKWNKWLRSRGRKRELRMSSTPTGLADVKGAP  63
QY      61  AQTLLRPQDMKMGASRPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLHAQ  120
Db      64  AQTLLRPQDMKMGASRPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLHAQ  123
QY      121  IYQFTDKDKNVAPRSKISPOGYGRRRRRSLPEAGPGRTLVSSKFPQAHGAPAPPS  175
Db      124  IYQFTDKDKNVAPRSKISPOGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA  178

RESULT 3
JN0766
adrenomedullin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1999
C:Accession: JN0766; P0610
R:Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo,
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A:Title: Molecular cloning and biological activities of rat adrenomedullin.
A:Reference number: JN0766; MUID:93384621
A:Accession: JN0766
A:Molecule type: mRNA
A:Residues: 1-185 <SAK>
A:Accession: P0610
A:Molecule type: protein
A:Residues: 22-41 <SA2>
C:Comment: This precursor contains a unique 20-amino acid sequence designated
essure control.
C:Keywords: amidated carboxyl end
F;1-21/domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted

```

E:94-143/Product: adrenomedullin #status predicted <MAT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

```

Query Match          65.9%;   Score 624.5;  DB 2;   Length 185;
Best Local Similarity 72.08;   Pred. No. 2.8e-50;
Matches 126;  Conservative 14;  Mismatches 32;  Indels 3;  Gaps 2;

Qy  1  VVSALMTYGLSLAFGADTARLDVASEFRKKWNKWLARGKRELRMSSSYTGLADYKAGP 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  4  VSIALMLGLSLAVLGADTARLDTSSQFRKKWNKWLARGKRELQAASSSYTGLVDEKTPV 63

Qy  61  AQTILRPDMKAGSRSPEDSPDARITRVKRYROSMNMFQGLRSGFRGCTCTVQKLAHQ 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  64  TQTLL-GLQDKOSTSTPQASTQSTAHIRVKRYRQSMN--QGSRSSTGCRFGCTCTWQKLAHQ 120

Qy  121  IYQFTDKDNVAPRSKISPOGYGRRRRRSIPEAGPGRTLTVSSKPOAHGAPAPPS 175
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  121  IYQFTDKDKGMAPRNKISPOGYGRRRRRSIPEVLRTAVTSSQEQTHSAPASPA 175

RESULT 4
T16112
hypochemical protein F20D12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16112
R:Wu, X
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F20D12.
A:Reference number: Z18462
A:Accession: T16112
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1116 <X>
A:Cross-references: EMBL:U40933; NID:g1072142; PID:g1072146; PIDN:AAA81675.1; CESP:F.2
C:Genetics:
A:Gene: CESP:F20D12.2
A:Introns: 21/1; 85/1; 175/3; 217/1; 361/3; 697/3; 891/1; 1008/1; 1072/1

Query Match          10.1%;   Score 95.5;  DB 2;   Length 1116;
Best Local Similarity 22.2%;   Pred. No. 1.2;
Matches 36;  Conservative 26;  Mismatches 63;  Indels 37;  Gaps 6;

Qy  46  SSSYP-TGLADVKA-----GPAQTLIRPDMKAGSRSPEDSPDAAIRIVKRYRQ 94
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  73  TSSPLKSGSDTKVPNLRGEFATRPQRMIPPAAGANSLFRPREGTPDGSSENRTNFQK 132

Qy  95  SMNPFQ-----LRSGFCRFGCTCTVQKLAHQIYQFTDKDNVAPRSK 137
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  133  NLNDIKSEAPLGKYNFQSGFRKDIKSF---FGRAK-PKTEESIDETHVIKKEAPPSM 188

Qy  138  I-----SPQGYGRRRRRSIPEAGPGRTLTVSSKPOAHGAPAPP 174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  189  FGVTLAAPKFGFSITSLTEKPSISIKFSGSMKPSRSSPAPP 230

RESULT 5
S34427
tristetrapoline protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S34427
R:Taylor, G.A.; Lai, W.S.; Oakey, R.J.; Seldin, M.F.; Shows, T.B.; Eddy Jr., R.L.; Bli
Nucleic Acids Res. 19, 3454, 1991
A:Title: The human TTP protein: sequence, alignment with related proteins, and chromo
A:Reference number: S34427; MUID:91288233
A:Accession: S34427
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-326 <TAY>
A:Cross-references: EMBL:MG3625; NID:g340012; PIDN:AAA61240.1; PID:g340013
C:Keywords: DNA binding
```

Query Match 9.5%; Score 89.5; DB 2; Length 326;
Best Local Similarity 22.4%; Pred. No. 1.1;
Matches 45; Conservative 18; Mismatches 77; Indels 61; Gaps 8;

QY 34 WALSRGKRLRMSSVPTGLADVKAGPAQTLIRPQD-----MKGASRPE 78
DB 32 WG-SSGFWLSLSPSDSPSGVTSRLFGRTSLVEGRSCGWVPPPGFAPLAPRLGPELSPS 90
QY 79 DSSPDAARIVRKVRQSMNMFQGLRSEF---CRFGT-CTV-----QK 116
DB 91 PTSPPTATSTPSPRYKTEL-----CRFSESGRVCGAKQFAHGLGELRQANRHPKYKTE 145
QY 117 LAHQIYQ-----FTDKDKNVAP-----RSKISPGQVGRRRRRSLPAGPGR 158
DB 146 LCHKFYLQGRCPYGRCHETHNPESDLAAPHVPLRQISFSGPLSGRRTSPPPPLAG 205
QY 159 TLVSSKPOAHGAPAPPGSSAP 179
DB 206 PSLSSSSSPSSPPPPGDL 226

RESULT 6
KFHUS
coagulation factor V precursor [validated] - human
N;Alternate names: coagulation labile factor; proaccelerin
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change 08-Dec-2000
C;Accession: A56172; A42344; A28028; A27498; A25897
R;Cripe, L.D.; Moore, K.D.; Kane, W.H.
Biochemistry 31, 3777-3785, 1992
A;Title: Structure of the gene for human coagulation factor V.
A;Reference number: A42344; MUID:92232668
A;Accession: A56172
A;Molecule type: DNA
A;Residues: 1-224 <CR>
A;Cross-references: GB:J05368
A;Accession: A42344

A;Molecule type: mRNA
A;Residues: 48-58;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-542;
2070;2111-2120;2172-2181 <CR2>
R;Jenny, R.J.; Pittman, D.D.; Toole, J.J.; Kriz, R.W.; Aldape, R.A.; Hewick, R.M.; Kaufm
Proc. Natl. Acad. Sci. U.S.A. 84, 4846-4850, 1987
A;Title: Complete cDNA and derived amino acid sequence of human factor V.
A;Reference number: A28028; MUID:87260886
A;Accession: A28028
A;Molecule type: mRNA
A;Residues: 1-857,'R',859-864,'R',866-924,'E',926-1763,'I',1765-2212,'T',2214-2224 <JEN>
A;Cross-references: GB:M16967
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Kane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W.
Biochemistry 26, 6508-6514, 1987
A;Title: Cloning of cDNAs coding for the heavy chain region and connecting region of hum
A;Reference number: A27498; MUID:88107560
A;Accession: A27498
A;Molecule type: mRNA
A;Residues: 1-1284,'I',1286-1600 <KAN>
A;Cross-references: GB:M17785
A;Note: parts of this sequence were determined by protein sequencing
R;Kane, W.H.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 6800-6804, 1986
A;Title: Cloning of a cDNA coding for human factor V, a blood coagulation factor homolog
A;Reference number: A25897; MUID:86313665
A;Accession: A25897
A;Molecule type: mRNA
A;Residues: 1188-1215,1315-2224 <KA2>
A;Cross-references: GB:M14335
A;Note: parts of this sequence were determined by protein sequencing
R;Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
Biochemistry 34, 4118-4124, 1995
A;Title: Thrombin-catalyzed activation of recombinant human factor V.
A;Reference number: A56139; MUID:95210278
A;Contents: annotation; thrombin cleavage sites

C;Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
C;Genetics:
A;Gene: GDB:F5
A;Cross-references: GDB:119896; OMIM:227400
A;Map position: 1q23-1q23
A;Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1;
C;Function:
A;Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa p
A;Pathway: blood coagulation
C;Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase
C;Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plasm
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-224/Product: coagulation factor V #status predicted <MAT>
F:29-737/Product: coagulation factor Va heavy chain #status experimental <VAH>
F:29-345/Domain: A1 <DA1>
F:33-329/Domain: ferroxidase repeat homology <FO1>
F:346-691/Domain: A2 <DA2>
F:351-684/Domain: ferroxidase repeat homology <FO2>
F:692-1573/Domain: B <DOB>
F:1183-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
F:1574-2224/Product: coagulation factor Va light chain #status experimental <VAL>
F:1574-1905/Domain: A3 <DA3>
F:1581-1905/Domain: ferroxidase repeat homology <FO3>
F:1667-1765/Region: phospholipid binding #status predicted
F:1906-2061/Domain: discoidin I amino-terminal homology <DN1>
F:2065-2224/Domain: C2 <DC2>
F:2065-2221/Domain: discoidin I amino-terminal homology <DN2>
F:5155-239,297,460,468,554,741,752,760,776,782,821,936,977,1074,1083,1103,1106,1479,
F:167-193,248-329,500-526,603-684,1725-1751,1907-2061,2066-2221/Disulfide bonds: #sta
F:334-335/Cleavage site: Arg-Asn (protein C) #status predicted
F:363,693,1546/Binding site: sulfate (Tyr) (covalent) #status predicted
F:376-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
F:382,1338/Binding site: carbohydrate (Asn) (covalent) #status absent
F:534-535/Cleavage site: Arg-Gly (protein C) #status predicted
F:737-738/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experiment
F:1046-1047/Cleavage site: Arg-Thr (coagulation factor Xa, thrombin) #status experime
F:1573-1574/Cleavage site: Arg-Ser (thrombin) #status experimental

Query Match 9.4%; Score 89; DB 1; Length 2224;
Best Local Similarity 23.2%; Pred. No. 10;
Matches 39; Conservative 26; Mismatches 71; Indels 32; Gaps 5;

QY 3 VALMYLGLSLAFLGADTAR-----LDVASEPRKKWNKWLRSRGKRELMSSTPTGLAD 55
DB 847 IRLSLGAGEFKSOEHAHKHKPKVERDQAARKHFSWMKLLAHKVGRLHSQDTGSPSGMRP 906
QY 56 VKAGPAQTLIRPQDMKGASRSPED-----SSPDAARIVRKVRQSMNMFQGLRSGFRGT 111
DB 907 WEDLPSTQDTGSPSRMRPWKDPSPSDLLLLKQSNSSKTLVGRWHLAS----- 951
QY 112 CTVQKLAHQIYQTDKDKDNVAPRSKISPGYGRRRRRSLPEAG-PGR 158
DB 952 ---EKSGYEIIQ--DTDEDTAVNNWLISPNQNASRAWGESTPLANKPGK 994

RESULT 7
T52311
isopenicillin N epimerase [validated] - Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52311
R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
J. Bacteriol. 172, 3952-3958, 1990
A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deaceto
A;Reference number: Z26033; MUID:90299822
A;Accession: T52311
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-398 <KOV>
A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
C;Genetics:
A;Gene: cefD

Db 310 FFRATAGKEPVRSXEYKLRADGSW-AWVIDGQPRFSADGCTFLGYVGVSLDITERRAAE- 367

QY 65 IRPQDMKGASRPEDSSPDAAIRVKRYRQSMNNOGLSFRCFGTCTVQKLAHOIYOF 124

Db 368 IAOQEAQAFIRSIIDSDPCVIRLMEGRPLLMNEAGRRIIFGLNEGAPVTGQTWDSIGRA 427

QY 125 TDKXDKNVAPRSKISPGVGRRRRSLPEAGPCRTL--YSSKP--QAHGAP 171

Db 428 SDADKVEAAWES--VRRGKTARFEISVRDAGGEERCMDVISAPITDHHGK 476

RESULT 13

JH0190

alpha-2-adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997

C:Accession: JH0190

R:Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.

Mol. Cell. Biochem. 97, 161-172, 1990

A:Title: Molecular cloning, sequencing and expression of an alpha2-adrenergic receptor

A:Reference number: JH0190; MUID:91125329

A:Accession: JH0190

A:Molecule type: mRNA

A:Residues: 1-450 <CHA>

A:Experimental source: brain

C:Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It me

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:34-59/Domain: hydrophobic <HDI>

F:71-96/Domain: hydrophobic <HII>

F:106-131/Domain: hydrophobic <III>

F:150-175/Domain: hydrophobic <HIV>

F:193-218/Domain: hydrophobic <HDV>

F:375-400/Domain: hydrophobic <HVI>

F:405-430/Domain: hydrophobic <VII>

Query Match 8.7%; Score 82.5; DB 2; Length 450;

Best Local Similarity 25.5%; Pred. No. 6.9; 73; Indels 21; Gaps 7;

Matches 40; Conservative 23; Mismatches

QY 33 KWALSRGKRELRLSSSYPTGLADYKAGPAQTLIRPQDMKGASRPEDSSPDAAIRVKRY 92

Db 140 EYNLKRTRRIKAITHCVVISAVISFPLISI--EKKGAGGQQPAEPSCKINDQKWY 196

QY 93 ROSMNNFOGLRFGRCFGTCTVQKLAH-QIYQFTDKDKNVAPRSK-----ISPGYGRR 146

Db 197 VIS-----SSIGSFAPCLIMLVYRIYQIA-KRRTRVPPSRRGPDACAPPGGADR 248

QY 147 RRRSL-PEAGPGRTLVSCKP--QAHGAPAPPSGSAK 179

Db 249 RPNLGPBERGAGTAGGEAPLPTQLNGAPGEFAPTRP 285

RESULT 14

F88632

protein F56B3.4 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: F88632

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A:Accession: F88632

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-926 <STO>

A:Cross-references: GB:chr_IV; PIDN:AAO02615.1; PID:G2854201; GSPDB:GN00022; CESP:F56

C:Genetics:

A:Gene: F56B3.4

A:Map position: 4

Search completed: October 17, 2002, 15:22:41
Job time : 18.1922 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 31.4202 Seconds
(without alignments)
643.390 Million cell updates/sec

Title: US-10-018-924-2_COPY_4_185
Perfect score: 947
Sequence: 1 VSVALLYLGLSLAFLGADTAR.....SKPQAHGAPAPSGSAPHFLL 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
A_Geneseq_032802.*			
1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*		
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*		
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*		
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*		
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*		
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*		
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*		
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*		
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*		
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*		
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*		
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*		
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15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*		
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21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*		
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	947	100.0	185	22	Human adrenomedull
2	947	100.0	185	22	Human adrenomedull
3	817	86.3	188	22	Porcine adrenomedu
4	817	86.3	188	22	Porcine adrenomedu
5	624.5	65.9	185	22	Rat adrenomedullin
6	624.5	65.9	185	22	Rat adrenomedullin
7	469	49.5	97	21	Human secreted pro
8	305.5	32.3	120	22	USPA(1-57)-(A)-(GS
9	298	31.5	147	22	USPA(1-84)-(A)-(GS
10	297.5	31.4	120	22	USPA(1-56)-(DD)-(G
11	289	30.5	53	22	Glycine extended h

12	289	30.5	53	22	AA75112	Glycine extended a
13	289	30.5	62	22	AA75113	Linker peptide-adr
14	289	30.5	170	22	AA75114	Thiorodoxin-(GSGSG
15	283	29.9	52	22	AA75110	Human adrenomedull
16	283	29.9	52	22	AA91759	Human adrenomedull
17	283	29.9	52	22	AAE09818	Human adrenomedull
18	239	25.2	48	22	AA91763	Adrenomedullin pep
19	231	24.4	50	22	AAE09819	Rat adrenomedullin
20	227	24.0	52	22	AA91765	Adrenomedullin pep
21	219.5	23.2	53	22	AA91767	Adrenomedullin pep
22	196	20.7	40	22	AA91768	Adrenomedullin pep
23	181.5	19.2	37	22	AA91761	Adrenomedullin pep
24	176	18.6	33	22	AA91764	Adrenomedullin pep
25	163	17.2	31	18	AAW25160	Human preproadreno
26	163	17.2	31	22	AA91762	Human adrenomedull
27	163	17.2	31	22	AAE09827	Human adrenomedull
28	107	11.3	20	18	AAW25161	Human proadrenomed
29	104	11.0	20	22	AA91766	Adrenomedullin pep
30	97	10.2	20	22	AA91769	Adrenomedullin pep
31	89.5	9.5	326	22	AA71705	Human TRP protein.
32	89	9.4	2224	17	AAW04254	Human Factor V. H
33	89	9.4	2224	20	AA49564	Human lipoprotein
34	88.5	9.3	926	19	AAW44883	Chimeric polyproli
35	87.5	9.2	177	22	AA63878	Human prostate can
36	86.5	9.1	500	16	AA72590	Acromonium chrysog
37	86.5	9.1	654	20	AA26901	Amphotrophic MLV r
38	85	9.0	647	20	AA26907	Novel human diago
39	82	8.7	145	22	ABG05153	*polyproline beta-
40	81.5	8.6	167	19	AAW44910	Novel human diago
41	81.5	8.6	318	22	ABG19764	Murine leukaemia v
42	81.5	8.6	458	18	AAW26323	Envelope glycoprot
43	81.5	8.6	624	20	AA26913	Murine leukemia vi
44	81.5	8.6	625	22	AA919881	Murine leukemia vi
45	81.5	8.6	637	22	AA919878	Murine leukemia vi

ALIGNMENTS

RESULT 1
AA49697
ID AA49697 standard; Protein; 185 AA.
XX
AC AA49697;
XX
DT 04-APR-2001 (first entry)
XX
DE Human adrenomedullin amino acid sequence.
XX
KW Passive elongation; vesicle smooth muscle; uropathic activity;
KW adrenomedullin; urinary disorder; incontinence; human.
XX
OS Homo sapiens.
XX
PN WO200078338-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-JP04166.
XX
PR 23-JUN-1999; 99JP-0177549.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PY Yanagita T;
XX
DR WPI: 2001-080754/09.
DR N-PSDB; AA29138.
XX
PT Composition for promoting passive elongation of vesicle smooth muscle
PT comprises adrenomedullin
XX
PS Claim 1; Page 26-27; 42pp; Japanese.

XX This invention relates to a composition for promoting passive elongation
CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC uterine contraction activity. The composition can be used for promoting passive
CC elongation of vesicle smooth muscles, this is useful for relieving
CC urinary disorders such as impending urinary incontinence, reflex urinary
CC incontinence and urinary incontinence with overflow. The present sequence
CC represents the human adrenomedullin protein, which is used in the
CC composition of the invention.

SQ Sequence 185 AA;
Query Match 100.0%; Score 947; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-93;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSVLMYLGSLAFLGADTARLDVASEFRKKWNKWLRSKRLRMSSSYPTGLADVKAGP 60
DB 4 VSVLMYLGSLAFLGADTARLDVASEFRKKWNKWLRSKRLRMSSSYPTGLADVKAGP 63
QY 61 AQTLRPQDMKGASRPEDSSPDAAIRVKRYRQSMNPFQGLRSFGCRFGTCTVOKLAHQ 120
DB 64 AQTLRPQDMKGASRPEDSSPDAAIRVKRYRQSMNPFQGLRSFGCRFGTCTVOKLAHQ 123
QY 121 IQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPOAHGAPPPSGSAPH 180
DB 124 IQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPOAHGAPPPSGSAPH 183
QY 181 FL 182
DB 184 FL 185

RESULT 2
AAB60344
ID AAB60344 standard; Protein; 185 AA.

XX AAB60344;
XX
DT 06-APR-2001 (first entry)
XX Human adrenomedullin precursor.
XX Human; adrenomedullin; precursor; bradykinin antagonist;
KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW dysmenorrhoea; obstetric; gynaecological.

XX Homo sapiens.
XX WO200078339-A1.
XX 28-DEC-2000.
XX 23-JUN-2000; 2000WO-JP04167.
XX 23-JUN-1999; 99JP-0177548.
XX 21-MAR-2000; 2000JP-0079171.
XX (SHIO) SHIONOGI & CO LTD.

XX Yanagita T;
XX WPI; 2001-080755/09.
XX N-PSDB; AAF27228.

XX Composition for inhibiting automatic uterine contraction or contraction
PT caused by bradykinin comprises adrenomedullin -
XX Claim 7; Page 37-38; 54pp; Japanese.

XX The invention relates to a composition containing adrenomedullin for
CC inhibiting automatic uterine contraction or contraction caused by
CC bradykinin. The invention also relates to the use of adrenomedullin in

CC the preparation of a drug for preventing premature birth or miscarriage.
CC The composition of the invention can be used for preventing premature
CC birth, preventing miscarriage, stopping delivery before caesarean
CC section or for treating dysmenorrhoea. The present sequence
XX represents human adrenomedullin precursor.

SQ Sequence 185 AA;
Query Match 100.0%; Score 947; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-93;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSVLMYLGSLAFLGADTARLDVASEFRKKWNKWLRSKRLRMSSSYPTGLADVKAGP 60
DB 4 VSVLMYLGSLAFLGADTARLDVASEFRKKWNKWLRSKRLRMSSSYPTGLADVKAGP 63
QY 61 AQTLRPQDMKGASRPEDSSPDAAIRVKRYRQSMNPFQGLRSFGCRFGTCTVOKLAHQ 120
DB 64 AQTLRPQDMKGASRPEDSSPDAAIRVKRYRQSMNPFQGLRSFGCRFGTCTVOKLAHQ 123
QY 121 IQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPOAHGAPPPSGSAPH 180
DB 124 IQFTDKDKDNVAPRSKISPOGYGRRRRSLPEAGPGRTLVSSKPOAHGAPPPSGSAPH 183
QY 181 FL 182
DB 184 FL 185

RESULT 3
AAB49698
ID AAB49698 standard; Protein; 188 AA.

XX AAB49698;
XX
DT 04-APR-2001 (first entry)
XX Porcine adrenomedullin amino acid sequence.
XX Passive elongation; vesicle smooth muscle; uropathic activity;
KW adrenomedullin; urinary disorder; incontinence; proctine.

XX Sus scrofa.
XX WO200078338-A1.
XX 28-DEC-2000.
XX 23-JUN-2000; 2000WO-JP04166.
XX 23-JUN-1999; 99JP-0177549.
XX (SHIO) SHIONOGI & CO LTD.
XX Yanagita T;
XX WPI; 2001-080754/09.
XX N-PSDB; AAF29139.

XX Composition for promoting passive elongation of vesicle smooth muscle
PT comprises adrenomedullin -
XX Disclosure; Page 31-33; 42pp; Japanese.

XX This invention relates to a composition for promoting passive elongation
CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC uterine contraction activity. The composition can be used for promoting passive
CC elongation of vesicle smooth muscles, this is useful for relieving
CC urinary disorders such as impending urinary incontinence, reflex urinary
CC incontinence and urinary incontinence with overflow. The present sequence
CC represents the porcine adrenomedullin protein, which is used in the
CC composition of the invention.


```
SQ Sequence 188 AA;
Query Match 86.3%; Score 817; DB 22; Length 188;
Best Local Similarity 89.1%; Pred. No. 1.9e-79;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSVALLMYLGLSLAFLGADTARLDVASEFRKKWKNKVALSRGKRELRLSSSYPTGIADLKAGP 60
D 4 VPVALMYLGLSLAFLGADTARLDVAAEFRRKKWKNKVALSRGKRELRLSSSYPTGIADLKAGP 63

QY 61 AQTILRPQDMKGASRSPEDSSPDAAIRIVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQ 120
D 64 AQTIVRPQDMKGASRSPEDSSPDAAIRIVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQ 123

QY 121 IYQFTDKDKDNVAPRSKISPOQYGRRRRSRLPEAGPGRTLVSKKPOAHGAPAPPS 175
D 124 IYQFTDKDKDNVAPRSKISPOQYGRRRRSRLPEASLGRTLRSOEPOAHGAPASPA 178

RESULT 4
AAB60345
ID AAB60345 standard; Protein; 188 AA.
XX
AC AAB60345;
DT 06-APR-2001 (first entry)
DE Porcine adrenomedullin precursor.
XX
KW Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW dysmenorrhoea; obstetric; gynaecological.
XX
OS Sus scrofa.
XX
PN WO200078339-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-JP04167.
XX
PR 23-JUN-1999; 95JP-0177548.
XX
PR 21-MAR-2000; 2000JP-0079171.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Yanagita T;
XX
DR WPI; 2001-080755/09.
DR N-PSDB; AAF27229.
XX
PT Composition for inhibiting automatic uterine contraction or contraction
PT caused by bradykinin comprises adrenomedullin -
XX
PS Disclosure; Page 43-44; 54pp; Japanese.
XX
CC The invention relates to a composition containing adrenomedullin for
CC inhibiting automatic uterine contraction or contraction caused by
CC bradykinin. The invention also relates to the use of adrenomedullin in
CC the preparation of a drug for preventing premature birth or miscarriage.
CC The composition of the invention can be used for preventing premature
CC birth, preventing miscarriage, stopping delivery before caesarean
CC section or for treating dysmenorrhoea. The present sequence
CC represents porcine adrenomedullin precursor.
XX
SQ Sequence 188 AA;
Query Match 86.3%; Score 817; DB 22; Length 188;
Best Local Similarity 89.1%; Pred. No. 1.9e-79;
Matches 156; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSVALLMYLGLSLAFLGADTARLDVASEFRKKWKNKVALSRGKRELRLSSSYPTGIADLKAGP 60
D 4 VPVALMYLGLSLAFLGADTARLDVAAEFRRKKWKNKVALSRGKRELRLSSSYPTGIADLKAGP 63

QY 61 AQTILRPQDMKGASRSPEDSSPDAAIRIVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQ 120
D 64 AQTIVRPQDMKGASRSPEDSSPDAAIRIVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQ 123

QY 121 IYQFTDKDKDNVAPRSKISPOQYGRRRRSRLPEAGPGRTLVSKKPOAHGAPAPPS 175
D 124 IYQFTDKDKDNVAPRSKISPOQYGRRRRSRLPEASLGRTLRSOEPOAHGAPASPA 178

RESULT 5
AAB49699
ID AAB49699 standard; Protein; 185 AA.
XX
AC AAB49699;
DT 04-APR-2001 (first entry)
DE Rat adrenomedullin amino acid sequence.
XX
KW Passive elongation; vesicle smooth muscle; uropathic activity;
KW adrenomedullin; urinary disorder; incontinence; rat.
XX
OS Rattus norvegicus.
XX
PN WO200078338-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-JP04166.
XX
PR 23-JUN-1999; 95JP-0177549.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Yanagita T;
XX
DR WPI; 2001-080754/09.
DR N-PSDB; AAF29140.
XX
PT Composition for promoting passive elongation of vesicle smooth muscle
PT comprises adrenomedullin -
XX
PS Disclosure; Page 37-38; 42pp; Japanese.
XX
CC This invention relates to a composition for promoting passive elongation
CC of vesicle smooth muscle. The composition contains adrenomedullin, and has
CC uropathic activity. The composition can be used for promoting passive
CC elongation of vesicle smooth muscles, this is useful for relieving
CC urinary disorders such as impending urinary incontinence, reflex urinary
CC incontinence and urinary incontinence with overflow. The present sequence
CC represents the porcine adrenomedullin rat, which is used in the
CC composition of the invention.
XX
SQ Sequence 185 AA;
Query Match 65.9%; Score 624.5; DB 22; Length 185;
Best Local Similarity 72.0%; Pred. No. 8e-59;
Matches 126; Conservative 14; Mismatches 32; Indels 3; Gaps 2;

QY 1 VSVALLMYLGLSLAFLGADTARLDVASEFRKKWKNKVALSRGKRELRLSSSYPTGLADYKAGP 60
D 4 VSIALLMYLGLSLAFLGADTARLDTSQFRKKWKNKVALSRGKRELRLSSSYPTGLVDEKTPV 63

QY 61 AQTILRPQDMKGASRSPEDSSPDAAIRIVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQ 120
D 64 TOTL-GLQDKQSTSTSPQASTQSTAHIRVRYRQSMNN--QGSRSTGCRFGTCTMOKLAHQ 120

QY 121 IYQFTDKDKDNVAPRSKISPOQYGRRRRSRLPEAGPGRTLVSKKPOAHGAPAPPS 175
D 121 IYQFTDKDKDNVAPRSKISPOQYGRRRRSRLPEVLRARTVESSEQETHSAPASPA 175
```

RESULT 6
 AAB60346
 ID AAB60346 standard; Protein; 185 AA.
 KW AAB60346;
 AC AAB60346;
 XX AAB60346;
 XX AAB60346;
 DT 06-APR-2001 (first entry)
 DE Rat adrenomedullin precursor.
 DE Rat; adrenomedullin; precursor; bradykinin antagonist;
 KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
 KW dysmenorrhea; obstetric; gynaecological.
 XX Rattus norvegicus.
 OS Rattus norvegicus.
 FN WO200078339-A1.
 PN 28-DEC-2000.
 PD 23-JUN-2000; 2000WO-JP04167.
 XX 23-JUN-1999; 99JP-0177548.
 PR 21-MAR-2000; 2000JP-0079171.
 XX (SHIO) SHIONOGI & CO LTD.
 PA Yanagita T;
 XX WPI: 2001-080755/09.
 DR N-PSDB; AAF7230.
 XX Composition for inhibiting automatic uterine contraction or contraction
 PT caused by bradykinin comprises adrenomedullin -
 PT Disclosure; Page 48-49; 54pp; Japanese.
 PS The invention relates to a composition containing adrenomedullin for
 CC inhibiting automatic uterine contraction or contraction caused by
 CC bradykinin. The invention also relates to the use of adrenomedullin in
 CC the preparation of a drug for preventing premature birth or miscarriage.
 CC The composition of the invention can be used for preventing premature
 CC birth, preventing miscarriage, stopping delivery before caesarean
 CC section or for treating dysmenorrhea. The present sequence
 CC represents rat adrenomedullin precursor.
 XX Sequence 185 AA;
 SQ Query Match 65.9%; Score 624.5; DB 22; Length 185;
 Best Local Similarity 72.0%; Pred. No. 8e-59;
 Matches 126; Conservative 14; Mismatches 32; Indels 3; Gaps 2;
 QY 1 VSVAlMYGLSLAFGLGADTARLDVASEFRKKWNKWLSSRGKRELRMSSSYPTGLADYKAGP 60
 DB 4 VSIAlMLLGLSLAVLGADTARLDTSQQPRKKWNKWLSSRGKRELQASSSYPTGLVDEKTPV 63
 QY 61 AQTILRPQDMKGASRSPEDSSPDAAIRVRYRQSMNFGQLRSFCGFCGTCVQKLAHQ 120
 DB 64 TQTLL-GLQDKQSTSSTPQASTQTAHIVRYRQSMN--QGSRSSTGCGFCGTCVQKLAHQ 120
 QY 121 IYQFTDQKQVAPRSKISPGQYGRRRRRSLPAGPGTGLVSSKPOAHGAPAPPS 175
 DB 121 IYQFTDQKQVAPRNKISPGQYGRRRRRSLPEVLRTVSSQEQTHSPASPA 175
 RESULT 7
 AAG00251
 ID AAG00251 standard; Protein; 97 AA.
 KW AAG00251;
 AC AAG00251;
 XX AAG00251;
 DT 06-OCT-2000 (first entry)

DT 31-JUL-2001 (first entry)
XX Linker peptide-adrenomedullin (AM) precursor protein.
DE
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
KW
XX Homo sapiens.
OS Synthetic.
OS
XX WO200127310-A1.
PN
XX 19-APR-2001.
PD
XX 10-OCT-2000; 2000WO-JP07023.
PF
XX 15-OCT-1999; 99JP-0294147.
PR (SHIO) SHIONOGI & CO LTD.
XX
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI
XX WPI; 2001-282044/29.
DR N-PSDB; AAH19809.
DR
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
PT
XX Claim 20; Page 48; 75pp; Japanese.
PS
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 62 AA;
Query Match 30.5%; Score 289; DB 22; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.8e-23;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 92 YRQSMNFGRLSRGCRFGCTVQKLAHQIYQFTDKDKNVAPRSKISPOGYG 144
Db 10 YRQSMNFGRLSRGCRFGCTVQKLAHQIYQFTDKDKNVAPRSKISPOGYG 62
RESULT 14
AAB75114
ID AAB75114 standard; Protein; 170 AA.
XX
XX AAB75114;
AC
XX 31-JUL-2001 (first entry)
DT
XX Thiorodoxin-(GSGSGDAFE)-AM-gly protein.
XX
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
KW
XX Homo sapiens.
OS Synthetic.
OS
XX WO200127310-A1.
PN
XX 19-APR-2001.
PD
XX 10-OCT-2000; 2000WO-JP07023.
PF

XX 15-OCT-1999; 99JP-0294147.
PR (SHIO) SHIONOGI & CO LTD.
XX
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI
XX WPI; 2001-282044/29.
DR N-PSDB; AAH19810.
DR
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
PT
XX Claim 17; Page 49-50; 75pp; Japanese.
PS
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 170 AA;
Query Match 30.5%; Score 289; DB 22; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.8e-23;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 92 YRQSMNFGRLSRGCRFGCTVQKLAHQIYQFTDKDKNVAPRSKISPOGYG 144
Db 118 YRQSMNFGRLSRGCRFGCTVQKLAHQIYQFTDKDKNVAPRSKISPOGYG 170
RESULT 15
AAB75110
ID AAB75110 standard; Protein; 52 AA.
XX
XX AAB75110;
AC
XX 31-JUL-2001 (first entry)
DT
XX Human adrenomedullin (AM) protein.
DE
XX
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
KW
XX Homo sapiens.
OS
XX WO200127310-A1.
PN
XX 19-APR-2001.
PD
XX 10-OCT-2000; 2000WO-JP07023.
PF
XX 15-OCT-1999; 99JP-0294147.
PR (SHIO) SHIONOGI & CO LTD.
XX
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
PI
XX WPI; 2001-282044/29.
DR N-PSDB; AAH19806.
DR
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
PT
XX Disclosure; Page 45; 75pp; Japanese.
PS
XX

CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
XX exemplification of the present invention.

SQ Sequence 52 AA;

Query Match 29.9%; Score 283; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.4e-23;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 YRQSMNFGRLRSFGCGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 143
Db 1 YRQSMNFGRLRSFGCGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52

Search completed: October 17, 2002, 15:21:13
Job time : 31.4202 secs

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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 6.51466 Seconds
(without alignments)
742.931 Million cell updates/sec

Title: US-10-018-924-2_COPY_22_146
Perfect score: 655
Sequence: 1 ARLDVASEFRKKNKWLRS.....FTDKDKDNVAPRSKISPOGY 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	655	100.0	185	1 ADML_HUMAN	P53318 homo sapien
2	611	93.3	188	1 ADML_PIG	P53366 sus scrofa
3	606	92.5	188	1 ADML_BOVIN	O62827 bos taurus
4	597	91.1	188	1 ADML_CANIS	O77559 canis famli
5	458.5	70.0	185	1 ADML_RAT	P43145 rattus norv
6	414	63.2	184	1 ADML_MOUSE	P97297 mus musculu
7	77	11.8	591	1 PTRR_MOUSE	P41593 mus musculu
8	75	11.5	591	1 PTRR_RAT	P25961 rattus norv
9	71.5	10.9	477	1 FIBB_PETMA	P02678 petromyzon
10	71	10.8	2224	1 FA5_HUMAN	P12259 homo sapien
11	69	10.5	454	1 PR11_SCHPO	O14215 schizosacch
12	68.5	10.5	479	1 FIBB_RAT	P14480 rattus norv
13	68.5	10.5	3144	1 VP13_YEAST	O07878 saccharomyc
14	67.5	10.3	300	1 MOXJ_METEX	P16028 methyllobact
15	67	10.2	436	1 SL56_BRAOL	P07761 brassica ol
16	67	10.2	457	1 TBA_DICDI	P32255 dictyosteli
17	66	10.1	380	1 GBB_MAIZE	P49178 zea mays (m
18	66	10.1	397	1 SK18_YEAST	O02793 saccharomyc
19	65.5	10.0	400	1 GUN5_BACAG	O85465 bacillus ag
20	65.5	10.0	448	1 TBA2_SCHCO	P49741 schizophyll
21	65.5	10.0	451	1 TBA2_EMENI	P24634 emericella
22	65.5	10.0	497	1 SC14_YARLI	P45816 varrowia li
23	65.5	10.0	532	1 TYRO_RANNI	O04604 rana nigroma
24	65	9.9	442	1 TOP5_BPT4	P07065 bacterioph
25	65	9.9	485	1 GLR_RAT	P30082 rattus norv
26	65	9.9	573	1 EYA3_HUMAN	O99504 homo sapien
27	65	9.9	1252	1 RPOB_CHLMU	P56869 chlamydia m
28	65	9.9	1252	1 RPOB_CHLTR	O84317 chlamydia t
29	65	9.9	3210	1 CENF_HUMAN	P49454 homo sapien
30	64.5	9.8	409	1 GUN2_BACSA	P06565 bacillus sp
31	64.5	9.8	491	1 FIBB_HUMAN	P02675 homo sapien
32	64.5	9.8	905	1 YD83_HUMAN	O9p294 homo sapien
33	63.5	9.7	397	1 CEF2_STRCL	P18549 streptomyce

34	63.5	9.7	458	1 A2AC_MOUSE	Q01337 mus musculu
35	63.5	9.7	458	1 A2AC_RAT	P22086 rattus norv
36	63.5	9.7	477	1 GLR_HUMAN	P47871 homo sapien
37	63.5	9.7	677	1 SPOT_HAEIN	P43811 haemophilus
38	63.5	9.7	980	1 SYN_DROME	Q24546 drosophila
39	63	9.6	215	1 Y457_ANASP	P29713 anabaena sp
40	63	9.6	440	1 GAT4_MOUSE	Q08369 mus musculu
41	63	9.6	459	1 G33_RAT	P05432 rattus norv
42	63	9.6	463	1 FIBB_CHICK	Q02020 gallus gall
43	63	9.6	995	1 DBPA_YEAST	Q12389 saccharomyc
44	62.5	9.5	108	1 SVS4_MOUSE	P18419 mus musculu
45	62.5	9.5	360	1 VP3_ARMV	P24820 arabis mosa

ALIGNMENTS

RESULT 1	ADML_HUMAN	STANDARD;	PRT;	185 AA.
AC	P35318;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20			
DE	terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].			
GN	ADM OR AM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pheochromocytoma;			
RX	MEDLINE=93343928; PubMed=7688224;			
RA	Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;			
RT	"Cloning and characterization of cDNA encoding a precursor for human			
RT	adrenomedullin.";			
RL	Biochem. Biophys. Res. Commun. 194:720-725(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=94354869; PubMed=8074714;			
RA	Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,			
RA	Kitamura K., Eto T., Matsuo H.;			
RT	"Genomic structure of human adrenomedullin gene.";			
RL	Biochem. Biophys. Res. Commun. 203:631-639(1994).			
RN	[3]			
RP	SEQUENCE OF 95-146.			
RC	TISSUE=Pheochromocytoma;			
RX	MEDLINE=93249425; PubMed=8387282;			
RA	Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,			
RA	Matsuo H., Eto T.;			
RT	"Adrenomedullin: a novel hypotensive peptide isolated from human			
RT	pheochromocytoma.";			
RL	Biochem. Biophys. Res. Commun. 192:553-560(1993).			
RN	[4]			
RP	REVIEW.			
RX	MEDLINE=98240137; PubMed=9578982;			
RA	Samson W.K.;			
RT	"Proadrenomedullin-derived peptides.";			
RL	Front. Neuroendocrinol. 19:100-127(1998).			
RN	[5]			
RP	REVIEW.			
RX	MEDLINE=20053666; PubMed=10588445;			
RA	Champion H.C., Nussdorfer G.G., Kadowitz P.J.;			
RT	"Structure-activity relationships of adrenomedullin in the circulation			
RT	and adrenal gland.";			
RL	Regul. Pept. 85:1-8(1999).			
CC	-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR			
CC	AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE			
CC	PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE			
CC	KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP			

CC INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
CC PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
CC INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
CC AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
CC ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
CC VESSELS.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
CC ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
CC TISSUES.
CC
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC
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CC
CC EMBL; D14874; BAA03589.1; -
CC EMBL; S73906; AAC60642.1; -
CC EMBL; D43639; BAA07756.1; ALT_SEQ.
CC PIR; JN0476; JN0476.
CC PIR; JN0684; JN0684.
CC PIR; JC2351; JC2351.
CC MIM; 103275; -
CC InterPro; IPR001710; Adrenomedullin.
CC Pfam; PF02039; Adrenomedullin; 1.
CC PRINTS; PR00801; ADRENOMEDULLIN.
CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
CC SIGNAL 1 21
CC PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
CC PROPEP 22 41
CC PROPEP 45 92
CC PEPTIDE 95 146
CC PROPEP 148 185
CC PEPTIDE 110 115
CC DISULFID 110 115
CC MOD_RES 41 41
CC MOD_RES 146 146
CC AMIDATION (G-42 PROVIDE AMIDE GROUP).
CC AMIDATION (G-147 PROVIDE AMIDE GROUP).
CC SEQUENCE 185 AA; 20420 MW; 64C7D2A0B4654DFE CRC64;
CC
CC Query Match 100.0%; Score 655; DB 1; Length 185;
CC Best Local Similarity 100.0%; Pred. No. 1e-61;
CC Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 ARLDVASEFRKKWKWALSRGKRELMSSTPTGLADYKAGPAQTILIRPQDMKGASRSPE 60
CC 22 ARLDVASEFRKKWKWALSRGKRELMSSTPTGLADYKAGPAQTILIRPQDMKGASRSPE 81
CC
CC Db 61 DSSPDAARIRVKRYRQSMNFFGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
CC 82 DSSPDAARIRVKRYRQSMNFFGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141
CC
CC QY 121 SPQGY 125
CC 142 SPQGY 146
CC
CC Db 121 SPQGY 125
CC 142 SPQGY 146
CC
CC RESULT 2
CC ADML_PIG
CC AC P53366; STANDARD; PRT; 188 AA.
CC
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
CC DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
CC CN ADM OR AM.
CC OS Eukarya; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NCBI_TaxID=9823;
CC RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-Adrenal medulla;
RX MEDLINE-94130945; PubMed-8043068;
RA Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT "Complete amino acid sequence of porcine adrenomedullin and cloning
of cDNA encoding its precursor.";
RL FEBS Lett. 338:306-310(1994).
RN [2]
RP SEQUENCE OF 22-41.
RC TISSUE-Adrenal medulla;
RX MEDLINE-94357274; PubMed-8076689;
RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT "Identification and hypotensive activity of proadrenomedullin
N-terminal 20 peptide (PAMP).";
RL FEBS Lett. 351:35-37(1994).
CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC AGENTS.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
CC KIDNEY.
CC
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC
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CC
CC EMBL; D14875; BAA03590.1; -
CC InterPro; IPR001710; Adrenomedullin.
CC Pfam; PF02039; Adrenomedullin; 1.
CC PRINTS; PR00801; ADRENOMEDULLIN.
CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
CC SIGNAL 1 21
CC PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
CC PROPEP 22 41
CC PROPEP 45 92
CC PEPTIDE 95 146
CC PROPEP 153 188
CC
CC DISULFID 110 115
CC MOD_RES 41 41
CC MOD_RES 146 146
CC AMIDATION (G-42 PROVIDE AMIDE GROUP).
CC AMIDATION (G-147 PROVIDE AMIDE GROUP).
CC SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;
CC
CC Query Match 93.3%; Score 611; DB 1; Length 188;
CC Best Local Similarity 91.2%; Pred. No. 4.4e-57;
CC Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 ARLDVASEFRKKWKWALSRGKRELMSSTPTGLADYKAGPAQTILIRPQDMKGASRSPE 60
CC 22 ARLDVASEFRKKWKWALSRGKRELMSSTPTGLADYKAGPAQTILIRPQDMKGASRSPE 81
CC
CC QY 61 DSSPDAARIRVKRYRQSMNFFGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
CC 82 ASIPDAARIRVKRYRQSMNFFGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141
CC
CC QY 121 SPQGY 125
CC 142 SPQGY 146
CC
CC Db 121 SPQGY 125
CC 142 SPQGY 146
CC
CC RESULT 3
CC ADML_BOVIN
CC ID ADML_BOVIN STANDARD; PRT; 188 AA.
CC AC O62827;
CC
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
CC DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].


```
GN ADML
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Norta;
RX MEDLINE=98244567; PubMed=9585168;
RA Barker S., Wood E., Clark A.J.L., Corder R.;
RT "Cloning of bovine proadrenomedullin and inhibition of its basal
RT expression in vascular endothelial cells by staurosporine.";
RL Life Sci. 62:1407-1415(1998).
CC -!- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CC CIRCULATION CONTROL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC -----
DR EMBL: AJ001613; CAA04866.1; -
DR InterPro: IPR001710; Adrenomedullin.
DR Pfam: PF02039; Adrenomedullin; 1.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 92 BY SIMILARITY.
FT PEPTIDE 95 146 ADRENOMEDULLIN.
FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
FT SIMILARITY).
FT DISULFID 110 115 BY SIMILARITY.
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;
Query Match 92.5%; Score 606; DB 1; Length 188;
Best Local Similarity 92.0%; Pred. No. 1.5e-56;
Matches 115; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 ARLDVASEFRKKWKNKVALSRGKRELMSSSYPPTGLADVAGPAQTILRPQDMKGASRSPE 60
DB 22 ARLDVASEFRKKWKNKVALSRGKRELMSSSYPPTGLADVAGPAQTILRPQDMKGASRSPE 81
QY 61 DSSPDAARIRVKRYROSMNFGRLSFGCRFGCTCTVQKLAHQIYQFTDKDKONVAPRSKI 120
DB 82 ASSPDAARIRVKRYROSLNFGRLSFGCRFGCTCTVQKLAHQIYHFTDKDKGSAAPRSKI 141
QY 121 SPOGY 125
DB 142 SPOGY 146
RESULT 4
ADML_CANFA STANDARD; PRT; 188 AA.
AC 077559; Q9TVCS;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (PROAM-N20) (PROAM N-terminal 20 peptide) (PAMP)].
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
```

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OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Imoto I., Jougasaki M.;
RT "Cloning of cDNA encoding canine adrenomedullin.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99002704; PubMed=9788655;
RA Ono Y., Kojima M., Okada K., Kangawa K.;
RT "cDNA cloning of canine adrenomedullin and its gene expression in the
RT heart and blood vessels in endotoxin shock.";
RL Shock 10:243-247(1998).
CC -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
CC AGENTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC -----
DR EMBL: AF045773; RAD05423.1; -
DR EMBL: U96127; AAD09957.1; -
DR InterPro: IPR001710; Adrenomedullin.
DR Pfam: PF02039; Adrenomedullin; 1.
KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
FT PROPEP 45 92 BY SIMILARITY.
FT PEPTIDE 95 146 ADRENOMEDULLIN.
FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
FT SIMILARITY).
FT DISULFID 110 115 BY SIMILARITY.
FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
FT CONFLICT 130 130 N -> K (IN REF. 2).
FT SEQUENCE 188 AA; 20929 MW; 809D6A64F98F5578 CRC64;
Query Match 91.1%; Score 597; DB 1; Length 188;
Best Local Similarity 90.4%; Pred. No. 1.3e-55;
Matches 113; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 ARLDVASEFRKKWKNKVALSRGKRELMSSSYPPTGLADVAGPAQTILRPQDMKGASRSPE 60
DB 22 ARLDVASEFRKKWKNKVALSRGKRELMSSSYPPTGLADVAGPAQTILRPQDMKGASRSPE 81
QY 61 DSSPDAARIRVKRYROSMNFGRLSFGCRFGCTCTVQKLAHQIYQFTDKDKONVAPRSKI 120
DB 82 TSGPDAARIRVKRYROSMNFGRLSFGCRFGCTCTVQKLAHQIYQFTDKDKONVAPRSKI 141
QY 121 SPOGY 125
DB 142 SPOGY 146
RESULT 5
ADML_RAT STANDARD; PRT; 185 AA.
AC P43145;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (PROAM-N20) (PROAM N-terminal 20 peptide) (PAMP)].
GN ADM.
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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX MEDLINE=93384621; PubMed=7690563;
RA Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA Matsuo H., Eto T.;
RT "Molecular cloning and biological activities of rat adrenomedullin, a
RT hypotensive peptide";
RL Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96102137; PubMed=8524787;
RA Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA Sulpiuzio A.C., Aliyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT its role in exacerbating focal brain ischemic damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC AGENTS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
CC HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC -----
DR EMBL; D15069; BAA03665.1; -.
DR EMBL; U15419; AAB60519.1; -.
DR InterPro: IPR001710; Adrenomedullin.
DR Pfam: PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
DR HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PROPEP 22 41
FT PROPEP 45 91
FT PEPTIDE 94 143
FT PROPEP 149 185
FT DISULFID 107 112
FT MOD_RES 41 41
FT MOD_RES 143 143
FT MOD_RES 143 143
FT SEQUENCE 185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;
Query Match 70.0%; Score 458.5; DB 1; Length 185;
Best Local Similarity 72.8%; Pred. No. 4.3e-41;
Matches 91; Conservative 10; Mismatches 21; Indels 3; Gaps 2;
QY 1 ARLDVASEFRKKWKNWALSRGKRELNRSSSYPTGLADVKAGPAQTLIRPQDMKAGSRSP 60
Db 22 ARLDTSOFRKKWKNWALSRGKRELNRSSSYPTGLVDEKVTPTQTL-GLQDKQSTSTPP 80
QY 61 DSSPDARIRVKRYRQSMNNFQGLRSFCRGCTCTVOKLAHQIYQFTDKDKNVAPRSKI 120
Db 81 ASTOSTAHIRVKRYRQSMN--QGSRSYTCRGCTCTMQLAHQIYQFTDKDGNAPRNKI 138
QY 121 SPQGY 125
Db 139 SPQGY 143

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RESULT 6
ADML_MOUSE STANDARD; PRT; 184 AA.
AC P97297; P97453;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN ADM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97092892; PubMed=8938454;
RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT "Genomic organization, expression, and chromosomal mapping of the
RT mouse adrenomedullin gene.";
RL Genomics 37:395-399(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Yotsumoto S., Ko M.S.H.;
RT "Expression of mouse adrenomedullin gene in trophoblastic giant
RT cells at the implantation site.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
CC AGENTS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC -----
DR EMBL; D78349; BAA11367.1; -.
DR EMBL; U77630; AAB36535.1; -.
DR MGD; MGI:108058; Adm.
DR InterPro: IPR001710; Adrenomedullin.
DR Pfam: PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
DR HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT PROPEP 22 41
FT PROPEP 45 92
FT PEPTIDE 95 144
FT PROPEP 151 184
FT DISULFID 108 113
FT MOD_RES 41 41
FT MOD_RES 144 144
FT MOD_RES 173 173
FT CONFLICT 173 173 A -> G (IN REF. 2).
FT SEQUENCE 184 AA; 20764 MW; C88C99045A79C898 CRC64;
Query Match 63.2%; Score 414; DB 1; Length 184;
Best Local Similarity 68.9%; Pred. No. 2e-36;
Matches 84; Conservative 8; Mismatches 28; Indels 2; Gaps 1;
QY 4 DVASEFRKKWKNWALSRGKRELNRSSSYPTGLADVKAGPAQTLIRPQDMKAGSRSP 63
Db 25 DTPSQFRKKWKNWALSRGKRELNRSSSYPTGLADETTVPTQTLDPFLDEQNTGTGLQASN 84
QY 64 PDAARIRVKRYRQSMNNFQGLRSFCRGCTCTVOKLAHQIYQFTDKDKNVAPRSKIS 123

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Db 85 QSEAHIRVKRYQSMN--QGSRSNGCRGCTGCTFKLAHQIYQLTDDKDKGMAPRNKISQ 142
QY 124 GY 125
Db 143 GY 144

RESULT 7
PTRR_MOUSE STANDARD; PRT; 591 AA.
AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE Precursor (PTH/PTHr receptor).
GN PTHRI OR PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEHA;
RX MEDLINE=95034305; PubMed=7524627;
RA Karperien M., van Dijk T.B., Hoesijmakers T., Cremers F.,
RA "Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone
RT related peptide receptor mRNA in mouse postimplantation embryos
RT indicates involvement in multiple developmental processes.";
RL Mech. Dev. 47:29-42(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid
RT hormone/parathyroid hormone-related peptide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATES ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X78936; CAA5536.1; -
CC EMBL; L34611; AAA40011.1; -
CC EMBL; L34608; AAA40011.1; JOINED.
CC EMBL; L34607; AAA40011.1; JOINED.
CC EMBL; L34609; AAA40011.1; JOINED.
CC EMBL; L34610; AAA40011.1; JOINED.
CC HSSP; Q03431; 1BL1.
CC GCRDb; GCR_1005; -
CC GCRDb; GCR_1614; -
CC MGD; MGI:97801; Pthr.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm.2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

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DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 591
FT FT 188
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 214 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 591
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
FT CONFLICT 27 28
FT CONFLICT 464 465
FT CONFLICT 500 501
SQ SEQUENCE 591 AA; F7876F8D388BDDFD CRC64;

Query Match 11.8%; Score 77; DB 1; Length 591;
Best Local Similarity 32.5%; Pred. No. 1.6;
Matches 26; Conservative 12; Mismatches 28; Indels 14; Gaps 5;

QY 4 DVASEFRKKWNKWSRG-KRELRM-SSSY------TGLADY--RAG---PAQTLIRP 49
Db 465 EVQAEIRKSNRWTLALDFRKRKARSGSSSYSGPMAHTSVTVGPRAGLSPLSPRLP 524
QY 50 QDMKGASRSPEDSDPAARI 69
Db 525 ATTNHSQLPGHAKPGAPAI 544

RESULT 8
PTRR_RAT STANDARD; PRT; 591 AA.
AC P25961;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE Precursor (PTH/PTHr receptor).
GN PTHRI OR PTHR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=92212903; PubMed=1313566;
RA Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
RA Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "Expression cloning of a common receptor for parathyroid hormone and
RT parathyroid hormone-related peptide from rat osteoblast-like cells: a
RT single receptor stimulates intracellular accumulation of both cAMP
RT and inositol trisphosphates and increases intracellular free
RT calcium.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
RN [2]
RP SEQUENCE FROM N.A.

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FT DISULFID 212 212 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 216 216 (BY SIMILARITY).
FT DISULFID 216 216 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 220 304 (BY SIMILARITY).
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.
SQ SEQUENCE 477 AA; B8A95E7E32D09D18 CRC64;
Query Match 10.9%; Score 71.5; DB 1; Length 477;
Best Local Similarity 26.3%; Pred. No. 4.9;
Matches 36; Conservative 15; Mismatches 59; Indels 27; Gaps 7;
QY 2 RLDVASEFRKKKNW-----ALSRGKRELKMSSTPTGLADY-----KAGPAQTLIRPQ 50
DB 274 RVDGSSNFARDWNTYKAERFNIAFGNGKICNIPGEYWLGTVTVHOLTQKHTQOVLFDMS 333
QY 51 DMKG-----ASRSPEDSSPDAAIRVRKYRQSMNN--FOGLRSFGCRFGTCTQOKLAH 101
DB 334 DWEGSSVYQAQYASFRPENA-QGYRLWVEDYSGNAGNALLGATQLMGDNRTWTI----H 388
QY 102 QIYQFT--DKDKDNVAP 116
DB 389 NGMQFSTEDRDNDWNP 405
RESULT 10
FA5_HUMAN STANDARD; PRT; 2224 AA.
ID FA5_HUMAN
AC P12259; Q14285;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coagulation factor V precursor (Activated protein C cofactor).
GN F5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88107560; PubMed=1567832;
RA Cripe L.D., Moore K.D., Kane W.H.;
RT "Structure of the gene for human coagulation factor V.";
RL Biochemistry 31:3777-3785(1992).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=87260886; PubMed=3110773;
RA Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A.,
RA Hewick R.M., Kaufman R.J., Mann K.G.;
RT "Complete cDNA and derived amino acid sequence of human factor V.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
[3]
SEQUENCE OF 1-1600 FROM N.A.
RX MEDLINE=88107560; PubMed=2827731;
RA Kane W.H., Ichinose A., Hagen F.S., Davie E.W.;
RT "Cloning of cDNAs coding for the heavy chain region and connecting
RT region of human factor V, a blood coagulation factor with four types
RT of internal repeats.";
RL Biochemistry 26:6508-6514(1987).
[4]
SEQUENCE OF 1188-1215 AND 1315-2224 FROM N.A.
RX MEDLINE=86313665; PubMed=3092220;
RA Kane W.H., Davie E.W.;
RT "Cloning of a cDNA coding for human factor V, a blood coagulation
RT factor homologous to factor VIII and ceruloplasmin.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
[5]
PARTIAL SEQUENCE FROM N.A.
RC TISSUE-Fibroblast;
RX MEDLINE=93203619; PubMed=8454869;
RA Shen N.L.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
RA Edgington T.S.;

RT "The serine protease cofactor factor V is synthesized by
RT lymphocytes.";
RL J. Immunol. 150:2992-3001(1993).
[6]
RP Sulfation.
RX MEDLINE=94264012; PubMed=8204629;
RA Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
RA Kaufman R.J.;
RT "Posttranslational sulfation of factor V is required for efficient
RT thrombin cleavage and activation and for full procoagulant activity.";
RL Biochemistry 33:6952-6959(1994).
[7]
RP Sulfation.
RX MEDLINE=90366699; PubMed=2168225;
RA Hortic G.L.;
RT "Sulfation of tyrosine residues in coagulation factor V.";
RL Blood 76:946-952(1990).
[8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 2065-2224.
RX MEDLINE=20052169; PubMed=10586886;
RA Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
RA Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
RA Fuentes-Prior P.;
RT "Crystal structures of the membrane-binding C2 domain of human
RT coagulation factor V.";
RL Nature 402:434-439(1999).
[9]
RP VARIANT APCR GLN-534.
RX MEDLINE=94217810; PubMed=8164741;
RA Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
RA Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
RT "Mutation in blood coagulation factor V associated with resistance to
RT activated protein C.";
RL Nature 369:64-67(1994).
CC -!- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
CC WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
CC -!- SUBUNIT: Factor Va is composed of a heavy chain and a light
CC chain, noncovalently bound. The interaction between the two chains
CC is calcium-dependent.
CC -!- DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA
CC REPEATS.
CC -!- PTM: Thrombin activates factor V proteolytically to the active
CC cofactor, factor Va (formation of a heavy chain at the N-
CC terminus and a light chain at the C-terminus).
CC -!- PTM: Sulfation is required for efficient thrombin cleavage and
CC activation and for full procoagulant activity.
CC -!- DISEASE: OMEN PARAHOMOPHILIA, AN HEMORRHAGIC DIATHESIS, IS DUE
CC TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN F5 RESULTS IN A
CC FORM OF THROMBOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR
CC MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT
CC A SLIGHT THROMBOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
CC IMPLANTATION.
CC -!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF
CC 2 PLASTOCYANIN-LIKE REPEATS.
CC -!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L327779; AAB59401.1;
DR EMBL; L327755; AAB59401.1; JOINED.
DR EMBL; L32756; AAB59401.1; JOINED.
DR EMBL; L32757; AAB59401.1; JOINED.
DR EMBL; L32758; AAB59401.1; JOINED.
DR EMBL; L32759; AAB59401.1; JOINED.
DR EMBL; L32760; AAB59401.1; JOINED.
DR EMBL; L32761; AAB59401.1; JOINED.

DR EMBL; L32762; AAB59401.1; JOINED.
 DR EMBL; L32763; AAB59401.1; JOINED.
 DR EMBL; L32764; AAB59401.1; JOINED.
 DR EMBL; L32765; AAB59401.1; JOINED.
 DR EMBL; L32766; AAB59401.1; JOINED.
 DR EMBL; L32767; AAB59401.1; JOINED.
 DR EMBL; L32768; AAB59401.1; JOINED.
 DR EMBL; L32769; AAB59401.1; JOINED.
 DR EMBL; L32770; AAB59401.1; JOINED.
 DR EMBL; L32771; AAB59401.1; JOINED.
 DR EMBL; L32772; AAB59401.1; JOINED.
 DR EMBL; L32773; AAB59401.1; JOINED.
 DR EMBL; L32774; AAB59401.1; JOINED.
 DR EMBL; L32775; AAB59401.1; JOINED.
 DR EMBL; L32776; AAB59401.1; JOINED.
 DR EMBL; L32777; AAB59401.1; JOINED.
 DR EMBL; L32778; AAB59401.1; JOINED.
 DR EMBL; M16967; AAB52424.1; -
 DR EMBL; M14335; AAB59532.1; -
 DR PIR; A25897; A25897.
 DR PIR; A28028; A28028.
 DR PDB; 1CZS; 26-NOV-99.
 DR PDB; 1CZT; 26-NOV-99.
 DR PDB; 1CZV; 26-NOV-99.
 DR MIM; 134400; -
 DR MIM; 188055; -
 DR MIM; 227310; -
 DR MIM; 227400; -
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR000421; FA58_C.
 DR Pfam; PF00394; Cu-oxidase; 3.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR SMART; SM00231; FA58C; 2.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
 DR PROSITE; PS01285; FA58C.1; 2.
 DR PROSITE; PS01286; FA58C.2; 2.
 KW Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
 KW Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
 FT SIGNAL 1 28
 FT CHAIN 29 2224 COAGULATION FACTOR V.
 FT CHAIN 29 737 HEAVY CHAIN.
 FT PEPTIDE 738 1573 ACTIVATION PEPTIDE (CONNECTING REGION).
 FT CHAIN 1574 2224 LIGHT CHAIN.
 FT DOMAIN 30 329 F5/8 TYPE A 1.
 FT DOMAIN 30 193 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 203 329 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 348 684 F5/8 TYPE A 2.
 FT DOMAIN 348 526 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 536 684 PLASTOCYANIN-LIKE 4.
 FT DOMAIN 692 1573 B.
 FT DOMAIN 895 928 2 X 17 AA TANDEM REPEATS.
 FT REPEAT 895 911 1-1.
 FT REPEAT 912 928 1-2.
 FT SIMILAR 1135 1148 TO 14 AA REPEATS IN BOVINE FA5.
 FT DOMAIN 1185 1501 [TNP]-L-S-P-D-L-S-Q-T.
 FT REPEAT 1185 1193 2-1.
 FT REPEAT 1194 1202 2-2.
 FT REPEAT 1203 1211 2-3.
 FT REPEAT 1212 1220 2-4.
 FT REPEAT 1221 1229 2-5.
 FT REPEAT 1230 1238 2-6.
 FT REPEAT 1239 1247 2-7.
 FT REPEAT 1248 1256 2-8.
 FT REPEAT 1257 1265 2-9.
 FT REPEAT 1266 1274 2-10.
 FT REPEAT 1275 1283 2-11.
 FT REPEAT 1284 1292 2-12.
 FT REPEAT 1293 1301 2-13.
 FT REPEAT 1302 1310 2-14.
 FT REPEAT 1311 1319 2-15.
 FT REPEAT 1320 1328 2-16.
 FT REPEAT 1329 1337 2-17.

FT REPEAT 1338 1346 2-18.
 FT REPEAT 1347 1355 2-19.
 FT REPEAT 1356 1364 2-20.
 FT REPEAT 1365 1373 2-21.
 FT REPEAT 1374 1382 2-22.
 FT REPEAT 1383 1391 2-23.
 FT REPEAT 1392 1400 2-24.
 FT REPEAT 1401 1409 2-25.
 FT REPEAT 1410 1418 2-26.

Query Match 10.8%; Score 71; DB 1; Length 2224;
 Best Local Similarity 22.6%; Pred. NO. 30;
 Matches 28; Conservative 20; Mismatches 52; Indels 24; Gaps 3;

QY 4 DVASEFRKKWKKWALSRCGRKRLRMSSSYPTGLADVKAGPAQTLLIRPQDMKGNRSRPED-- 61
 DB 873 DQAAKRFSSWKKLLAHKVGRLHSQDTGSPGMRPMEDLPDSQDTGSPMRPMKDPSPDLL 932
 QY 62 --SSPDAAIRVKRYRQSMNNFQGLRSGCRFGTCTVCKLAHQIYQFTDKDKDNVAPRSK 119
 DB 933 LLKQSNSSKILVGRWHLAS-----EKGSYELIQ--DTDEDTAVNNWL 972
 QY 120 ISPQ 123
 DB 973 ISPQ 976

RESULT 11
 PRII_SCHPO
 ID PRII_SCHPO STANDARD; PRT; 454 AA.
 AC O14215;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Probable DNA primase small subunit (EC 2.7.7.-).
 GN SPAC6812.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL
 CC RNA PRIMERS FOR THE OKAZAKI FRAGMENTS MADE DURING DISCONTINUOUS
 CC DNA REPLICATION.
 CC -!- SUBUNIT: HETERODIMER OF A SMALL SUBUNIT AND A LARGE SUBUNIT.
 CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC PRIMASE SMALL SUBUNIT
 CC FAMILY.
 CC
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 CC -----
 CC EMBL; Z98531; CAB11078.1; -
 CC InterPro; IPR002755; DNA_primase_S.
 CC Pfam; PF01896; DNA_primase_S; 1.
 KW Transferase; DNA replication; DNA-directed RNA polymerase; Primosome.
 FT ACT_SITE 66 66 POTENTIAL.
 FT ACT_SITE 131 131 POTENTIAL.
 FT ACT_SITE 133 133 POTENTIAL.
 FT METAL 143 143 POTENTIAL.
 FT METAL 144 144 POTENTIAL.
 FT METAL 150 150 POTENTIAL.
 FT METAL 153 153 POTENTIAL.
 SQ SEQUENCE 454 AA; 52009 MW; 71526FFAF7C2BBFA CRC64;

Query Match 10.5%; Score 69; DB 1; Length 454;
 Best Local Similarity 24.4%; Pred. No. 8.4;
 Matches 32; Conservative 20; Mismatches 43; Indels 36; Gaps 6;

QY 4 DVASEFRKKW-----NKNK-----LSRGRKRLRMSSSYPTGLADYKAGPAQTLIRP 49
 DB 275 DLASLRKKWEVDPERSSKNKKSDIDTVLGS-----IASISPSVIAIAKQDIDVILYLP 330
 QY 50 -----QDMKGASRSPEDSSPDAAIRVKKVRSQNNFQGLRSFCRGCTGVQKLAHQ 102
 DB 331 RLDVEVSRHLNHLKSPFCVHPGTSCVCPIDIERMDSFNPLK-----VPTVNDLQOE 383
 QY 103 IYQFTDKDKDN 113
 DB 384 L-----DKNSQN 390

RESULT 12
 FIBB_RAT
 ID FIBB_RAT STANDARD; PRT; 479 AA.
 AC P14480;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=95143386; PubMed=7841303;
 RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
 RT "Cloning of the complete coding sequence of rat fibrinogen B beta
 chain cDNA: interspecies conservation of fibrin beta 15-42 primary
 structure.";
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).
 RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=84194000; PubMed=6232608;
 RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
 RT "Potential basis for regulation of the coordinately expressed
 fibrinogen genes: homology in the 5' flanking regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RX MEDLINE=89378771; PubMed=2673932;
 RA Eastman E.M., Gilula N.B.;
 RT "Cloning and characterization of a cDNA for the B beta chain of rat
 fibrinogen: evolutionary conservation of translated and
 3'-untranslated sequences.";
 RL Gene 79:151-158(1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.
 RC STRAIN-WISTAR; TISSUE=Liver;
 RX MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotti A.-M., Taroux P., Duquet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 liver regeneration.";
 RL Exp. Cell Res. 169:47-56(1987).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 CC -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC
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 CC
 CC EMBL; U05675; AAA64866.1; -;
 CC EMBL; M27220; AAA41160.1; -;
 CC EMBL; K01336; AAA98625.1; -;
 CC EMBL; M35602; AAA41159.1; -;
 CC PIR; A05299; A05299.
 CC PIR; PE0010; PE0010.
 CC HSP; P02675; 1FZE.
 CC InterPro; IPR002181; Fibrinogen_C.
 CC Pfam; PF00147; Fibrinogen_C; 1.
 CC SMART; SM00186; FBG; 1.
 CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Blood coagulation; Plasma; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
 FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
 FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 219 304 BY SIMILARITY.
 FT DISULFID 229 258 BY SIMILARITY.
 FT DISULFID 412 425 BY SIMILARITY.
 FT CARBOHYD 382 382 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
 FT CONFLICT 439 439 L -> Q (IN REF. 5).
 FT CONFLICT 441 441 S -> T (IN REF. 5).
 FT CONFLICT 445 445 S -> A (IN REF. 5).
 FT CONFLICT 457 467 R -> K (IN REF. 5).
 FT CONFLICT 475 475 V -> F (IN REF. 5).
 SQ SEQUENCE 479 AA; 54303 MW; EC86DB77C3E0EC0 CRC64;
 Query Match 10.5%; Score 68.5; DB 1; Length 479;
 Best Local Similarity 20.9%; Pred. No. 10;
 Matches 31; Conservative 23; Mismatches 63; Indels 31; Gaps 6;

QY 2 RLDVASEFRKKWKWALSRLG-----KRLRMSSSYPTGLADY-----KAGPAQTLIRP 49
 DB 273 RQDGSVDYFGKWDPPYKKGFGNIATNEDTKYGLPGEYWLGNKISQLTRIGPTELLIE 332
 QY 50 QDMKGASRSPEDSSPDAAIRVKKVRSQNNFQGLRSFCRG-----TCTVQKLA 100
 DB 333 EDKMG-DKVKAHYGGFTVQTEANKYQVSVNKYKTAGNALMEGASOLVGENRTMTI----- 387
 QY 101 HOIYQFTDKDKDN-----VAPRSKISPO 123
 DB 388 HNGMFFSTYDRNDGWTTPDRKQCSKE 415

RESULT 13
 VPS13_YEAST
 ID VPS13_YEAST STANDARD; PRT; 3144 AA.
 AC Q07878; O00040;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vacuolar protein sorting-associated protein VPS13.
 GN VPS13 OR SOIL OR ILL040C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;


```
CC -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
CC KINASE RECEPTOR (ZMPK1).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00268; CAA68375.1; -
DR EMBL; X03170; CAA26934.1; ALT_INIT.
DR PIR; A27827; A27827.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR000858; Stocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
DR SMART; SM00473; PAN.AP; 1.
KW Self-incompatibility; Glycoprotein; Polymorphism; Signal.
FT SIGNAL 1 31
FT CHAIN 32 436 S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 436 AA; 49779 MW; E2332635B885A515 CRC64;

Query Match 10.2%; Score 67; DB 1; Length 436;
Best Local Similarity 25.3%; Pred. No. 13;
Matches 42; Conservative 22; Mismatches 42; Indels 60; Gaps 11;

QY 2 RLDVASEFRKKWKWALSRGKRELWSSS-----YPTG--LADVKAGPAQTLLI 47
Db 128 RLPVVAEL-----LSGNFVMDRSSNDASEYLWQSFYPTDTLLPEMKLG----- 173

QY 48 RFQDMK-----GASRSPEDSPDAARIRVKRYRQSMNMF---OGL-----RS---FGCR 90
Db 174 --YDLKATGLNRLFTSWRSSDD--PSSGDFSYKLETRSLPEFYLWHGIFPMHRS GPWNGVR 229

QY 91 F-GTCTVQKLAHQIYQFTDKXD-----NVA PRSKIS PQGY 125
Db 230 FSGIPEDQKLSYMYNFTENSEBEVAYFRMTNNSIYSLTSLSEGY 275
```

Search completed: October 17, 2002, 15:21:36
Job time : 7.51466 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:13 ; Search time 11.8078 seconds
(without alignments)
1017.222 Million cell updates/sec

Title: US-10-018-924-2_COPY_22_146

Perfect score: 655

Sequence: 1 ARLDVASEFRKKWKNKALSR.....FTDKDKDNVAPRSKISPGQY 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	185	2 JN0684	adrenomedullin pre
2	611	93.3	188	2 S41600	adrenomedullin p
3	458.5	70.0	185	2 JN0766	adrenomedullin pre
4	77	11.8	591	2 S44203	parathyroid hormon
5	76	11.6	589	2 I59297	parathyroid hormon
6	75	11.5	591	2 I54195	parathyroid hormon
7	75	11.5	1051	2 C95367	conserved hypothet
8	71.5	10.9	479	2 A25052	fibrinogen beta ch
9	71	10.8	2224	1 KPHU5	coagulation factor
10	69	10.5	380	2 T08036	GTP-binding regula
11	69	10.5	454	2 T39017	probable DNA prima
12	68.5	10.5	328	2 A05299	fibrinogen beta ch
13	68.5	10.5	926	2 F88632	protein F56B3.4 [i
14	68.5	10.5	1196	2 H86389	hypothetical prote
15	68.5	10.5	3144	2 S84791	VPS13 protein - ye
16	68	10.4	168	2 T28776	hypothetical prote
17	68	10.4	347	2 T31120	rod shape-determin
18	68	10.4	858	2 T09344	probable phospholi
19	67.5	10.3	300	2 J00707	methanol oxidatio
20	67	10.2	436	2 A27827	S-locus-specific g
21	66.5	10.2	1766	2 S03701	14K protein - pea
22	66	10.1	380	2 T02085	GTP-binding protei
23	66	10.1	397	2 S30023	antiviral protein
24	66	10.1	731	2 JC7701	ARHGAP9 protein -
25	66	10.1	1050	2 S57488	fimbrial protein p
26	65.5	10.0	297	2 T47857	myb protein-like -
27	65.5	10.0	451	2 S13337	tubulin alpha-2 ch
28	65.5	10.0	497	2 S43745	phosphatidylinosit
29	65.5	10.0	532	2 JC1392	monophenol monooxy

30	65.5	10.0	727	2 AD1868	hypothetical prote
31	65.5	10.0	1116	2 T16112	hypothetical prote
32	65	9.9	253	2 H81690	conserved hypothet
33	65	9.9	305	2 T24283	hypothetical prote
34	65	9.9	380	2 S71574	tubulin alpha chai
35	65	9.9	428	2 G75453	hypothetical prote
36	65	9.9	485	2 J01957	glucagon receptor
37	65	9.9	867	2 G81856	membrane alanyl am
38	65	9.9	924	2 T06636	hypothetical prote
39	65	9.9	1017	2 PC4035	cell-cycle-depende
40	65	9.9	1252	2 H71529	DNA-directed RNA p
41	65	9.9	1252	2 G81686	DNA-directed RNA p
42	64.5	9.8	381	2 D70669	coenzyme F420-depe
43	64.5	9.8	409	2 B25156	cellulase (EC 3.2.
44	64.5	9.8	417	2 T51467	glucose 6 phosphat
45	64.5	9.8	444	2 T25413	hypothetical prote

ALIGNMENTS

RESULT 1

JN0684

adrenomedullin precursor - human

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence-revision 03-Feb-1994 #text_change 20-Jun-2000

C:Accession: JC2351; JN0684; P00548; JN0476

R:Shimizu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto,

Biochem. Biophys. Res. Commun. 203, 631-639, 1994

A:Title: Genomic structure of human adrenomedullin gene.

A:Reference number: JC2351; MUID:94354869

A:Accession: JC2351

A:Molecule type: DNA

A:Residues: 1-185 <ISH>

A:Cross-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330

A:Experimental source: pheochromocytoma

R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuoka, H.; Eto, T.

Biochem. Biophys. Res. Commun. 194, 720-725, 1993

A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome

A:Reference number: JN0684; MUID:93343928

A:Accession: JN0684

A:Molecule type: mRNA

A:Residues: 1-185 <KIT>

A:Cross-references: GB:D14874; NID:9455470; PIDN:BAA03589.1; PID:9500612

A:Accession: P00548

A:Molecule type: protein

A:Residues: 22-41 <KIT>

R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuoka, H.; Eto,

Biochem. Biophys. Res. Commun. 192, 553-560, 1993

A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocyt

A:Reference number: JN0476; MUID:93249425

A:Accession: JN0476

A:Molecule type: protein

A:Residues: 95-146 <KIT>

A:Experimental source: pheochromocytoma

C:Genetics:

A:Gene: GDB:ADM

A:Cross-references: GDB:217070; OMIM:103275

A:Map position: lipiter-lipiter

A:Introns: 33/2; 83/2

C:Keywords: amidated carboxyl end; blood pressure control; hormone

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-185/Product: proadrenomedullin #status predicted <PEU>

F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>

F:95-146/Product: adrenomedullin #status experimental <MAR>

F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following

F:110-115/Disulfide bonds: #status experimental

F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 100.0%; Score 655; DB 2; Length 185;

Best Local Similarity 100.0%; Pred. No. 2.6e-61;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARLDVASEFRKKWNKVALSRGKRELRMSSSYPTGLADVKGAGPAOTLIRPQDMKGASRSP 60
 DB 22 ARLDVASEFRKKWNKVALSRGKRELRMSSSYPTGLADVKGAGPAOTLIRPQDMKGASRSP 81
 QY 61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKI 120
 DB 82 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKI 141
 QY 121 SPQGY 125
 DB 142 SPQGY 146
 RESULT 2
 S41600
 adrenomedullin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S41600
 R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
 FEBS Lett. 338, 306-310, 1994
 A:Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encod
 A:Reference number: S41600; MUID:94139945
 A:Accession: S41600
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-188 <KIT>
 A:Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
 Query Match 93.3%; Score 611; DB 2; Length 188;
 Best Local Similarity 91.2%; Pred. No. 1.1e-56;
 Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ARLDVASEFRKKWNKVALSRGKRELRMSSSYPTGLADVKGAGPAOTLIRPQDMKGASRSP 60
 DB 22 ARLDVASEFRKKWNKVALSRGKRELRMSSSYPTGLADVKGAGPAOTLIRPQDMKGSSRSPQ 81
 QY 61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKI 120
 DB 82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVOKLAHQIYQFTDKDKDGVAPRSKI 141
 QY 121 SPQGY 125
 DB 142 SPQGY 146
 RESULT 3
 JN0766
 adrenomedullin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
 C:Accession: JN0766; P0610
 R:Kitamura, K.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T.
 Biochem. Biophys. Res. Commun. 195, 921-927, 1993
 A:Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
 A:Reference number: JN0766; MUID:93384621
 A:Accession: JN0766
 A:Molecule type: mRNA
 A:Residues: 1-185 <SAK>
 A:Accession: P0610
 A:Molecule type: protein
 A:Residues: 22-41 <SA2>
 C:Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
 assure control.
 C:Keywords: amidated carboxyl end
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-185/Product: proadrenomedullin #status predicted <PEU>
 F:22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
 F:94-143/Product: adrenomedullin #status predicted <MAT>
 F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
 F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

<hr/>					
Query Match	70.0%	Score 458.5;	DB 2;	Length 185;	
Best Local Similarity	72.8%;	Pred. No. 1.1e-40;			
Matches	91;	Conservative	10;	Mismatches	21; Indels 3; Gaps 2;
<hr/>					
Qy	1	ARLDVASEFRKKWKWALSRGKRELRLMSSSYPTGLADVACGPAQTLLRPDMKGASRSP	60		
Db	22	ARLDTSSQFRKKWKWALSRGKRELRLMSSSYPTGLDEKTVPTQLT-GLQDKOSTSTPQ	80		
<hr/>					
Qy	61	DSSPDAAIRVKRYRQSNNFQGRSGRCFTGCTVOKLAHQIYQFTDCKDNVAPRSKI	120		
Db	81	ASTOSTAHIRVKRYRQSN--QGSRSTGCRFGCTCMOKLAHQIYQFTDCKDKGMARNKI	138		
<hr/>					
Qy	121	SPQGY 125			
Db	139	SPQGY 143			
<hr/>					
RESULT 4					
S44203		parathyroid hormone-related peptide receptor - mouse			
C:Species:	Mus musculus (house mouse)				
C:Date:	13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000				
C:Accession:	S44203				
R:Karperien, M.; van Dijk, T.B.; Hoeljmackers, T.; Cremers, F.; Abou-Samra, A.B.; Boon					
submitted to the EMBL Data Library, April 1994					
A:Description:	Expression pattern of parathyroid hormone/parathyroid hormone related				
A:Reference number:	S44203				
A:Accession:	S44203				
A>Status:	preliminary				
A:Molecule type:	mRNA				
A:Residues:	1-591 <KAR>				
A:Cross-references:	EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829				
C:Superfamily:	glucagon receptor				
<hr/>					
Query Match	11.8%	Score 77;	DB 2;	Length 591;	
Best Local Similarity	32.5%;	Pred. No. 4.3;			
Matches	26;	Conservative	12;	Mismatches	28; Indels 14; Gaps 5;
<hr/>					
Qy	4	DVASEFRKKWKWALSRG-KRELRLM-SSSYP-----TGLADV--KAG---PAQTLIRP	49		
Db	465	EVQAEIRKWSRWTLALDFRKARKSGSSSYGPGMAHTSVTNVGPRAGLSPLSLPLLP	524		
<hr/>					
Qy	50	ODMKGASRPEDSDPAARI 69			
Db	525	ATTNGHSQLPGHAKPGAPAI 544			
<hr/>					
RESULT 5					
I59297		parathyroid hormone/parathyroid hormone related-peptide receptor - mouse			
C:Species:	Mus musculus (house mouse)				
C:Date:	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000				
C:Accession:	I59297				
R:McCuauig, K.A.; Clarke, J.C.; White, J.H.					
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994					
A>Title:	Molecular cloning of the gene encoding the mouse parathyroid hormone/parathy				
A:Reference number:	I59297; MUID:94255468				
A:Accession:	I59297				
A>Status:	preliminary; translated from GB/EMBL/DDBJ				
A:Molecule type:	DNA				
A:Residues:	1-589 <RES>				
A:Cross-references:	GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g530151				
C:Genetics:					
A:Gene:	PTH				
A:Introns:	25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;				
C:Superfamily:	glucagon receptor				
<hr/>					
Query Match	11.6%	Score 76;	DB 2;	Length 589;	
Best Local Similarity	32.5%;	Pred. No. 5.4;			
Matches	26;	Conservative	12;	Mismatches	28; Indels 14; Gaps 5;
<hr/>					
Qy	4	DVASEFRKKWKWALSRG-KRELRLM-SSSYP-----TGLADV--KAG---PAQTLIRP	49		
Db	4	DVASEFRKKWKWALSRG-KRELRLM-SSSYP-----TGLADV--KAG---PAQTLIRP	49		

Db	463	NVQAEIKKSWRTWLALDFKFKARSGSSSYSGPMPWVSHTSVTNVGPRAGLSLPLSPRLPLP	522
Qy	50	QDMKGASRSPEDSSPDAARI	69
Db	523	ATTNGHSQLPGHGAKPGAPAI	542

RESULT 6
I54195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C;Accession: I54195; A42698
R;Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (and rat genomes.
A;Reference number: I54195; MUID:94292182
A;Accession: I54195
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-591 <RES>
A;Cross-references: GB|L19475; NID:9467316; PIDN:AAA68098.1; PID:9467317
R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol trisphosphates and increases intracellular free calcium.
A;Reference number: A42698; MUID:92212903
A;Accession: A42698
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-585, 'G', 587-591 <ABO>
A;Experimental source: ROS 17/2.8 osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:92187)
C;Superfamily: glucagon receptor

Query Match	11.58;	Score 75;	DB 2;	Length 591;
Best Local Similarity	32.5%;	Pred. No. 6.9;		
Matches 25;	Conservative	12;	Mismatches	26;
			Indels	14;
			Gaps	5;

Qy	4	DVASEFRKKWNKWSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTILRP	49
		: : : : : : : : :	
Db	465	EVQAEIRKSWSRWTLALDFRKRRKARGSSSYSGPMVSHTSVTVNGPRAGLSLPSRLPP	524

Qy	50	QDMKGASRSPEDSSPDA	66
		: :	
Dd	525	ATTNGHSQPLGCHAKPGA	541

RESULT 7
C95367
conserved hypothetical protein Sma1548 [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95367
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95367

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 11051 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65501.1; PID:gi4523974; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid p5yMA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Neault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Smal548
A;Genome: plasmid

Query Match	11.5%	Score 75;	DB 2;	Length 1051;
Best Local Similarity	26.9%	Pred. No. 13;		
Matches	32;	Conservative 14;	Mismatches 63;	Indels 10;
Gaps				

QY	5	VASEFRKK-----WNKVALSRGKRELRMSS-----YPTGLADVKGAPQTLIRPQDMKNGAS	56
		: : : : : : : : : : : : : : : :	
Db	320	VRSEYRLRRADGWS-ARWIDVGQPRFSADGTFELGYGVSLDITERRAAE-IAQOEQAQAFI	377
		: : : : : : : : : : : : : : :	
QY	57	RSPEDSSPDAAARTVKRYRROSMNFCGLRSFGCRFGCTVQKLAHQIYQFTDRDKDNVA	115
		: : : : : : : : : : : : : : :	
Db	378	RSIFDSSPCDVRILDMEGRPFLLMNEAGRRTFGLNEGAPVTGQTDWISIGRASDADKVEAA	436
		: : : : : : : : : : : : : : :	

RESULT 8
A25052
fibrinogen beta chain - sea lamprey (fragments)
N:Contains: fibrinopeptide B
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 25-Oct-1987 #sequence.revision 19-feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; F03124
R:Bohnus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A:Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 19-479 <BOH>
A:Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
R:Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A:Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A:Reference number: A03120; MUID:77065679

A; Accession: A03124
A; Molecule type: protein
A; Residues: 1-36 <COT1>
A; Accession: B03124
A; Molecule type: protein
A; Residues: 37-42 <COT2>
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide ring homology
C; Keywords: blood coagulation; glycoprotein; sulfoprotein
F; 1-36/Product: fibrinopeptide B #status experimental <FPB>
F; 37-479/Product: fibrin beta chain #status experimental <MAT>
F; 90-219/Domain: fibrinogen disulfide ring homology <FDR>
F; 229-477/Domain: fibrinogen beta/gamma homology <FBG>
F; 13/Binding site: sulfate (Tyr) (covalent) #status experimental
F; 27/Binding site: carboxydrate (Asn) (covalent) #status experimental

Query Match	10.9%	Score	71.5;	DB	2;	Length	479;
Best Local Similarity	26.3%	Pred. No.	13;				
Matches	36;	Conservative	15;	Mismatches	59;	Indels	27;
Gaps							
QY	2	RLDVASERKKWKKW-----ALSRGKRELRMSSYPTGLADV----	KAGPAQTLIRPQ	50			
Db	276	KVDGSSNFARDWNTYKAEFGNIAFGNGKSGICNIPGEYWLGTTKVHQLTKQHTQQVLFDM	S	335			
QY	51	DMKG-----ASRPEDSSPDAARIVKRYRQSMNN--FQGLRSFGRCFTCTVQKLAH	101				
Db	336	DWEGSSVYAQYASFPENEA-QGYELWVEDYSGNAGNALLEGATQLMCDNFTMI----	H	390			
QY	102	QIQFT--DKDKNVAP	116				
Db	391	NGMQFSTFDRDNDNNWP	407				

RESULT 9
KFHU5
coagulation factor V precursor [validated] - human

	Best Local Similarity	24.0%; Pred. NO. 72;	Matches	30; Conservative	19; Mismatches	43; Indels	33; Gaps	7;
QY	3	LDVASEFRKKWNK--WALSRGKRELRMSSSYPTGLADVAKGAPQT-----L	46					
Db	19	VSVGALLTGSDWKYKSSRGKDRF--PYPGYKAVRAHSNGTYTMEIEGAKGLFL	74					
QV	47	IRPDMDKGRSPEDS-----SPDAAIRV---KRYRQSMNNEQGLRSGFCRGFTCTVQR	98					

Db 75 IRYLDESWGTGTPDIAMGKLOKTDPSHLKIWHGRFTCKMG---GMEFFG--FKNPLVQR 129
Qy 99 LAHQI 103
Db 130 LLREL 134

RESULT 15

S64791
VPS13 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L0901; protein YLL040c
C:Species: Saccharomyces cerevisiae
C:Date: 01-Aug-1995 #sequence.revision 24-May-1996 #text_change 13-Sep-1998
C:Accession: S64791; S64792; S14891
R:Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64775
A:Accession: S64791
A:Molecule type: DNA
A:Residues: 1-1360 <DUE>
A:Cross-references: EMBL:Z73145; MIPS:YLL040c
A:Experimental source: strain S288C
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64792
A:Molecule type: DNA
A:Residues: 1095-3144 <WED>
A:Cross-references: EMBL:Z73145; MIPS:YLL040c
A:Experimental source: strain S288C
R:Lombardo, A.; Carine, K.; Scheffler, I.E.
J. Biol. Chem. 265, 10419-10423, 1990
A:Title: Cloning and characterization of the iron-sulfur subunit gene of succinate dehydrogenase
A:Reference number: A35435; MUID:90285165
A:Accession: S14891
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 2991-3047, 'L' <LOM>
A:Cross-references: EMBL:J05487
C:Genetics:
A:Gene: SGD:VPS13; VPT2; SOI1
A:Cross-references: SGD:S0003963; MIPS:YLL040c
A:Map position: 12L
C:Function:
A:Description: involved in regulation of membrane traffic
C:Keywords: transmembrane protein
F:1084-1100/Domain: transmembrane #status predicted <TMM>

Query Match 10.5%; Score 68.5; DB 2; Length 3144;
Best Local Similarity 28.0%; Pred. No. 2e+02;
Matches 37; Conservative 20; Mismatches 36; Indels 39; Gaps 10;

Qy 19 SRGKRELRMSSPYTGLADVKGAPQTLIRPDNKGASRS---PE---DSSPDAAIR 70
Db 1354 SGGKEIKSPSPDPA SL-----SSSESTATPQSIQSGNKNKPEQYLDPSFKAPKIA 1409
Qy 71 VKRYRQ-----SMNN-----FQGLRSFGCRFG---TCTVQKLAHQIYQFTDKD----K 111
Db 1410 LTLNKTGVTSLNDCGLTRIMFQDI---GCSLGLKNDGTVDGOAH-VAAFRIEDVRNIK 1465
Qy 112 DN----VAPRSK 119
Db 1466 DNKHTLIPKSK 1477

Search completed: October 17, 2002, 15:22:40
Job time : 13.8078 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 21.5798 Seconds
(without alignments)
643.390 Million cell updates/sec

Title: US-10-018-924-2_COPY_22_146
Perfect score: 655
Sequence: 1 ARLDVASEFRKKWKNKVALSR.....FTDKDKDNVAPRSKISPGQY 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	100.0	185	22 AAB49697	Human adrenomedullin
2	655	100.0	185	22 AAB60344	Human adrenomedullin
3	611	93.3	188	22 AAB49698	Porcine adrenomedullin
4	611	93.3	188	22 AAB60345	Porcine adrenomedullin
5	458.5	70.0	185	22 AAB49699	Rat adrenomedullin
6	458.5	70.0	185	22 AAB60346	Rat adrenomedullin
7	384	58.6	97	21 AAG00251	Human secreted pro
8	299.5	45.7	120	22 AAB75122	UspA(1-57)-(A)-(GS
9	292	44.6	147	22 AAB75124	UspA(1-84)-(A)-(GS
10	291.5	44.5	120	22 AAB75123	UspA(1-56)-(DD)-(G
11	283	43.2	52	22 AAB75110	Human adrenomedullin

12	283	43.2	52	22 AAB91759	Adrenomedullin pep
13	283	43.2	52	22 AAE09818	Human adrenomedullin
14	283	43.2	53	22 AAB75111	Glycine extended h
15	283	43.2	53	22 AAB75112	Linker peptide-adr
16	283	43.2	62	22 AAB75113	Thioredoxin-(GSGSG
17	283	43.2	170	22 AAB75114	Adrenomedullin pep
18	239	36.5	48	22 AAB91763	Adrenomedullin pep
19	231	35.3	50	22 AAE09819	Rat adrenomedullin
20	227	34.7	52	22 AAB91765	Adrenomedullin pep
21	219.5	33.5	53	22 AAB91767	Adrenomedullin pep
22	196	29.9	40	22 AAB91768	Adrenomedullin pep
23	181.5	27.7	37	22 AAB91761	Adrenomedullin pep
24	163	24.9	31	18 AAB25160	Human preproadreno
25	163	24.9	31	22 AAB91762	Adrenomedullin pep
26	163	24.9	31	22 AAE09827	Human adrenomedullin
27	107	16.3	20	18 AAB25161	Human proadrenomed
28	104	15.9	20	22 AAB91766	Adrenomedullin pep
29	97	14.8	20	22 AAB91769	Adrenomedullin pep
30	75	11.5	435	21 AAB07529	A mutant parathyro
31	75	11.5	446	21 AAY96983	Tethered PTH-1 rec
32	75	11.5	591	13 AAR27706	Rat bone PTH/PTHrP
33	75	11.5	591	17 AAR92277	Parathyroid hormon
34	75	11.5	591	20 AAW73316	Human Factor V. H
35	71	10.8	2224	17 AAW04254	Human lipoprotein
36	71	10.8	2224	20 AAY49564	Novel human diagno
37	70.5	10.8	185	22 ABG05508	Protonibacterium
38	70	10.7	343	22 AAU82051	C glutamicum prote
39	69	10.5	783	22 AAG91263	Human protein SEQ
40	68.5	10.5	401	22 AAM79810	A human regulator
41	68.5	10.5	462	21 AAB18668	Human protein SEQ
42	68.5	10.5	462	22 AAM78826	Novel human diagno
43	68	10.4	515	22 ABG19073	Novel human diagno
44	68	10.4	651	22 ABG08359	Novel human diagno
45	68	10.4	944	22 ABG02404	Novel human diagno

ALIGNMENTS

RESULT 1
AAB49697
ID AAB49697 standard; Protein: 185 AA.
XX
AC AAB49697;
XX
DT 04-APR-2001 (first entry)
XX
DE Human adrenomedullin amino acid sequence.
XX
KW Passive elongation; vesicle smooth muscle; uropathic activity;
KW adrenomedullin; urinary disorder; incontinence; human.
XX
OS Homo sapiens.
XX
PN WO200078338-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-JP04166.
XX
PR 23-JUN-1999; 99JP-0177549.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Yanagita T;
XX
DR WPI; 2001-080754/09.
DR N-PSDB; AAF29138.
XX
PT Composition for promoting passive elongation of vesicle smooth muscle
PT comprises adrenomedullin -
XX
PS Claim 1; Page 26-27; 42pp; Japanese.


```

Db      22  ARLDVAEEFRKKWNKWSRGKRELRLSSSYPTGIADLKAGPAQTIVIRPDQVKGSSRSPQ 81
QY      61  DSSPDAARIRVKRYRQSMNMFQGLRSFGCGFTCTVQKLAHQIYQFTDKDKNVAPRSKI 120
Db      82  ASIPDAARIRVKRYRQSMNMFQGLRSFGCGFTCTVQKLAHQIYQFTDKDKNVAPRSKI 141
QY     121  SPQGY 125
Db     142  SPQGY 146

RESULT 4
AAB60345
ID  AAB60345 standard; Protein; 188 AA.
XX  AC  AAB60345;
XX  DT  06-APR-2001 (first entry)
XX  DE  Porcine adrenomedullin precursor.
XX  KW  Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
XX  KW  uterine contraction inhibitor; premature birth; miscarriage; abortion;
XX  KW  dysmenorrhea; obstetric; gynaecological.
XX  OS  Sus scrofa.
XX  PN  WO200078339-A1.
XX  PD  28-DEC-2000.
XX  PF  23-JUN-2000; 2000WO-JP04167.
XX  PR  23-JUN-1999; 99JP-0177548.
XX  PR  21-MAR-2000; 2000JP-0079171.
XX  PA  (SHIO ) SHIONOGI & CO LTD.
XX  PI  Yanagita T;
XX  WPI: 2001-080755/09.
XX  N-PSDB; AAF27229.
XX  PT  Composition for inhibiting automatic uterine contraction or contraction
XX  PT  caused by bradykinin comprises adrenomedullin
XX  PS  Disclosure; Page 43-44; 54pp; Japanese.
XX  CC  The invention relates to a composition containing adrenomedullin for
XX  CC  inhibiting automatic uterine contraction or contraction caused by
XX  CC  bradykinin. The invention also relates to the use of adrenomedullin in
XX  CC  the preparation of a drug for preventing premature birth or miscarriage.
XX  CC  The composition of the invention can be used for preventing premature
XX  CC  birth, preventing miscarriage, stopping delivery before caesarean
XX  CC  section or for treating dysmenorrhoea. The present sequence
XX  CC  represents porcine adrenomedullin precursor.
XX  SQ  Sequence 188 AA;

Query Match 93.3%; Score 611; DB 22; Length 188;
Best Local Similarity 91.2%; Pred. No. 3.1e-64;
Matches 114; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      1  ARLDVASEFRKKWNKWSRGKRELRLSSSYPTGLADVKGAGPAQTIVIRPDQVKGSSRSPQ 81
Db     22  ARLDVAAEFRKKWNKWSRGKRELRLSSSYPTGIADLKAGPAQTIVIRPDQVKGSSRSPQ 81
QY      61  DSSPDAARIRVKRYRQSMNMFQGLRSFGCGFTCTVQKLAHQIYQFTDKDKNVAPRSKI 120
Db      82  ASIPDAARIRVKRYRQSMNMFQGLRSFGCGFTCTVQKLAHQIYQFTDKDKNVAPRSKI 141
QY     121  SPQGY 125
Db     142  SPQGY 146

RESULT 5
AAB49699
ID  AAB49699 standard; Protein; 185 AA.
XX  AC  AAB49699;
XX  DT  04-APR-2001 (first entry)
XX  DE  Rat adrenomedullin amino acid sequence.
XX  KW  Passive elongation; vesicle smooth muscle; uropathic activity;
XX  KW  adrenomedullin; urinary disorder; incontinence; rat.
XX  OS  Rattus norvegicus.
XX  PN  WO200078338-A1.
XX  PD  28-DEC-2000.
XX  PF  23-JUN-2000; 2000WO-JP04166.
XX  PR  23-JUN-1999; 99JP-0177549.
XX  PA  (SHIO ) SHIONOGI & CO LTD.
XX  PI  Yanagita T;
XX  WPI: 2001-080754/09.
XX  N-PSDB; AAF29140.
XX  PT  Composition for promoting passive elongation of vesicle smooth muscle
XX  PT  comprises adrenomedullin
XX  PS  Disclosure; Page 37-38; 42pp; Japanese.
XX  CC  This invention relates to a composition for promoting passive elongation
XX  CC  of vesicle smooth muscle. The composition contains adrenomedullin, and has
XX  CC  uropathic activity. The composition can be used for promoting passive
XX  CC  elongation of vesicle smooth muscles, this is useful for relieving
XX  CC  urinary disorders such as impending urinary incontinence, reflex urinary
XX  CC  incontinence and urinary incontinence with overflow. The present sequence
XX  CC  represents the porcine adrenomedullin rat, which is used in the
XX  CC  composition of the invention.
XX  SQ  Sequence 185 AA;

Query Match 70.0%; Score 458.5; DB 22; Length 185;
Best Local Similarity 72.8%; Pred. No. 3.7e-46;
Matches 91; Conservative 10; Mismatches 21; Indels 3; Gaps 2;

QY      1  ARLDVASEFRKKWNKWSRGKRELRLSSSYPTGLADVKGAGPAQTIVIRPDQVKGSSRSPQ 60
Db     22  ARLDTSQFRRKKWNKWSRGKRELRLSSSYPTGLVDEKTVPTQL-GLQDKQSTSTFQ 80
QY      61  DSSPDAARIRVKRYRQSMNMFQGLRSFGCGFTCTVQKLAHQIYQFTDKDKNVAPRSKI 120
Db      81  ASTQSTAHIRVKRYRQSMN--QGSRSRSTGRCFTCTVQKLAHQIYQFTDKDKNVAPRSKI 138
QY     121  SPQGY 125
Db     139  SPQGY 143

RESULT 6
AAB60346
ID  AAB60346 standard; Protein; 185 AA.
XX  AC  AAB60346;
XX  DT  06-APR-2001 (first entry)

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```

Db      142  SPQGY 146

RESULT 5
AAB49699
ID  AAB49699 standard; Protein; 185 AA.
XX  AC  AAB49699;
XX  DT  04-APR-2001 (first entry)
XX  DE  Rat adrenomedullin amino acid sequence.
XX  KW  Passive elongation; vesicle smooth muscle; uropathic activity;
XX  KW  adrenomedullin; urinary disorder; incontinence; rat.
XX  OS  Rattus norvegicus.
XX  PN  WO200078338-A1.
XX  PD  28-DEC-2000.
XX  PF  23-JUN-2000; 2000WO-JP04166.
XX  PR  23-JUN-1999; 99JP-0177549.
XX  PA  (SHIO ) SHIONOGI & CO LTD.
XX  PI  Yanagita T;
XX  WPI: 2001-080754/09.
XX  N-PSDB; AAF29140.
XX  PT  Composition for promoting passive elongation of vesicle smooth muscle
XX  PT  comprises adrenomedullin
XX  PS  Disclosure; Page 37-38; 42pp; Japanese.
XX  CC  This invention relates to a composition for promoting passive elongation
XX  CC  of vesicle smooth muscle. The composition contains adrenomedullin, and has
XX  CC  uropathic activity. The composition can be used for promoting passive
XX  CC  elongation of vesicle smooth muscles, this is useful for relieving
XX  CC  urinary disorders such as impending urinary incontinence, reflex urinary
XX  CC  incontinence and urinary incontinence with overflow. The present sequence
XX  CC  represents the porcine adrenomedullin rat, which is used in the
XX  CC  composition of the invention.
XX  SQ  Sequence 185 AA;

Query Match 70.0%; Score 458.5; DB 22; Length 185;
Best Local Similarity 72.8%; Pred. No. 3.7e-46;
Matches 91; Conservative 10; Mismatches 21; Indels 3; Gaps 2;

QY      1  ARLDVASEFRKKWNKWSRGKRELRLSSSYPTGLADVKGAGPAQTIVIRPDQVKGSSRSPQ 60
Db     22  ARLDTSQFRRKKWNKWSRGKRELRLSSSYPTGLVDEKTVPTQL-GLQDKQSTSTFQ 80
QY      61  DSSPDAARIRVKRYRQSMNMFQGLRSFGCGFTCTVQKLAHQIYQFTDKDKNVAPRSKI 120
Db      81  ASTQSTAHIRVKRYRQSMN--QGSRSRSTGRCFTCTVQKLAHQIYQFTDKDKNVAPRSKI 138
QY     121  SPQGY 125
Db     139  SPQGY 143

RESULT 6
AAB60346
ID  AAB60346 standard; Protein; 185 AA.
XX  AC  AAB60346;
XX  DT  06-APR-2001 (first entry)

```

XX DE Rat adrenomedullin precursor.
 XX DE
 KW Rat; adrenomedullin; precursor; bradykinin antagonist;
 KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
 KW dysmenorrhoea; obstetric; gynaecological.
 XX OS
 XX Rattus norvegicus.
 XX PN WO200078339-A1.
 XX PD 28-DEC-2000.
 XX PF 23-JUN-2000; 2000WO-JP04167.
 XX PR 23-JUN-1999; 99JP-0177548.
 XX PR 21-MAR-2000; 2000JP-0079171.
 XX PA (SHIO) SHIONOGI & CO LTD.
 XX PI Yanagita T;
 DR WPI; 2001-080755/09.
 DR N-PSDB; AAF27230.
 PT Composition for inhibiting automatic uterine contraction or contraction
 PT caused by bradykinin comprises adrenomedullin -
 XX Disclosure; Page 48-49; 54pp; Japanese.
 XX The invention relates to a composition containing adrenomedullin for
 CC inhibiting automatic uterine contraction or contraction caused by
 CC bradykinin. The invention also relates to the use of adrenomedullin in
 CC the preparation of a drug for preventing premature birth or miscarriage.
 CC The composition of the invention can be used for preventing premature
 CC birth, preventing miscarriage, stopping delivery before caesarean
 CC section or for treating dysmenorrhoea. The present sequence
 CC represents rat adrenomedullin precursor.
 XX SQ Sequence 185 AA;
 Query Match 70.0%; Score 453.5; DB 22; Length 185;
 Best Local Similarity 72.8%; Pred. No. 3.7e-46;
 Matches 91; Conservative 10; Mismatches 21; Indels 3; Gaps 2;
 QY 1 ARLDVASEFRKKWKNWALSRGKRELMSSTPTGLADYKAGPAQTLIRPQDMKGASRSP 60
 DB 22 ARLDYSSQFRKKWKNWALSRGKRELQASSTPTGLVDEKTVPTQL-GLQDKQSTSTPQ 80
 QY 61 DSSPDAARIRVKRYRQSMNFGLSFGFCFTGCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
 DB 81 ASTQSTAHIRVKRYRQSMN--QGSRSFGCTGCTMQKLAHQIYQFTDKDKDGMAPRNKI 138
 QY 121 SPQGY 125
 DB 139 SPQGY 143
 RESULT 7
 AAG00251
 ID AAG00251 standard; Protein; 97 AA.
 AC AAG00251;
 XX 06-OCT-2000 (first entry)
 XX Human secreted protein, SEQ ID NO: 4332.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX Homo sapiens.
 OS

PN EP1033401-A2.
 XX 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-0200610.
 XX 26-FEB-1999; 99US-0122487.
 XX (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 DR N-PSDB; AAC00257.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 13; SEQ ID 4332; 71pp + CD-ROM; English.
 XX The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX SQ Sequence 97 AA;
 Query Match 58.6%; Score 384; DB 21; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.1e-37;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARLDVASEFRKKWKNWALSRGKRELMSSTPTGLADYKAGPAQTLIRPQDMKGASRSP 60
 DB 22 ARLDVASEFRKKWKNWALSRGKRELMSSTPTGLADYKAGPAQTLIRPQDMKGASRSP 81
 QY 61 DSSPDAARIRVKRYR 75
 DB 82 DSSPDAARIRVKRYR 96
 RESULT 8
 AAB75122
 ID AAB75122 standard; Protein; 120 AA.
 XX AAB75122;
 AC AAB75122;
 XX 31-JUL-2001 (first entry)
 XX UsPA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
 DE Adrenomedullin; glycine extended adrenomedullin; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200127310-A1.
 XX 19-APR-2001.
 XX 10-OCT-2000; 2000WO-JP07023.
 XX 15-OCT-1999; 99JP-0294147.

XX (SHIO) SHIONOGI & CO LTD.
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX WPI: 2001-282044/29.
XX N-PSDB; AAH19864.
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host
XX Claim 17; Page 68; 75pp; Japanese.
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX Sequence 120 AA;
XX Query Match 45.7%; Score 299.5; DB 22; Length 120;
XX Best Local Similarity 64.7%; Pred. No. 1.5e-27;
XX Matches 66; Conservative 3; Mismatches 12; Indels 21; Gaps 4;
QY 24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVRYRQSMNFG 83
DB 39 DVNYSPLY-TGLIDVNLG-----DMAGS-----GSGDAF-----EYRQSMNFG 77
QY 84 LRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGY 125
DB 78 LRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGY 119
RESULT 9
AAB75124
ID AAB75124 standard; Protein; 147 AA.
XX AAB75124;
XX 31-JUL-2001 (first entry)
XX UsPA(1-84)-(A)-(GSGGDAFE)-AM-gly protein.
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX Homo sapiens.
XX Synthetic.
XX WO200127310-A1.
XX 19-APR-2001.
XX 10-OCT-2000; 2000WO-JP07023.
XX 15-OCT-1999; 99JP-0294147.
XX (SHIO) SHIONOGI & CO LTD.
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX WPI: 2001-282044/29.
XX N-PSDB; AAH19866.
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host

XX Claim 17; Page 71; 75pp; Japanese.
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX Sequence 147 AA;
XX Query Match 44.6%; Score 292; DB 22; Length 147;
XX Best Local Similarity 57.0%; Pred. No. 1.5e-26;
XX Matches 65; Conservative 6; Mismatches 25; Indels 18; Gaps 3;
QY 24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRV 71
DB 39 DVNYSPLY-TGLIDVNLGDMQKRISSETHALTELSTNAGYPITETLAGSGGDAF----- 93
QY 72 KRYRQSMNPFQGLRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGY 125
DB 94 -EYRQSMNPFQGLRSFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGY 146
RESULT 10
AAB75123
ID AAB75123 standard; Protein; 120 AA.
XX AAB75123;
XX 31-JUL-2001 (first entry)
XX UsPA(1-56)-(DD)-(GSGGDAFE)-AM-gly protein.
XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX Homo sapiens.
XX Synthetic.
XX WO200127310-A1.
XX 19-APR-2001.
XX 10-OCT-2000; 2000WO-JP07023.
XX 15-OCT-1999; 99JP-0294147.
XX (SHIO) SHIONOGI & CO LTD.
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX WPI: 2001-282044/29.
XX N-PSDB; AAH19865.
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host
XX Claim 17; Page 69-70; 75pp; Japanese.
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the

CC exemplification of the present invention.

XX SQ Sequence 120 AA;
 Query Match 44.5%; Score 291.5; DB 22; Length 120;
 Best Local Similarity 63.7%; Pred. No. 1.3e-26;
 Matches 65; Conservative 3; Mismatches 13; Indels 21; Gaps 4;
 QY 24 ELRSSSYPTGLADVKAGPAOTLIRPQDMKASRPEDSSPDAAIRVKRYRQSMNFG 83
 Db 39 DVNYSULY-TGLIDVNLG-----DDGGS-----GSGDAF-----EYRQSMNFG 77
 QY 84 LRSFGCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 125
 Db 78 LRSFGCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 119

RESULT 11
 AAB75110
 ID AAB75110 standard; Protein; 52 AA.
 AC AAB75110;
 XX 31-JUL-2001 (first entry)
 DT Human adrenomedullin (AM) protein.
 DE Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW Adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 KW Homo sapiens.
 OS WO200127310-A1.
 PN 19-APR-2001.
 XX 10-OCT-2000; 2000WO-JP07023.
 PF 15-OCT-1999; 99JP-0294147.
 XX (SHIO) SHIONOGI & CO LTD.
 XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 WPI; 2001-282044/29.
 DR N-PSDB; AAH19806.

XX Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX Disclosure; Page 45; 75pp; Japanese.
 XX The present invention describes a method (M1) for producing
 CC adrenomedullin-precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC exemplification of the present invention.

XX SQ Sequence 52 AA;
 Query Match 43.2%; Score 283; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.5e-26;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 74 YRQSMNFGRLSFGCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 125
 Db 1 YRQSMNFGRLSFGCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 52

RESULT 12

AAB91759
 ID AAB91759 standard; Peptide; 52 AA.
 XX AAB91759;
 XX 22-JUN-2001 (first entry)
 DT Adrenomedullin peptide (AM) SEQ ID NO:935.
 DE Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2000069900-A2.
 PN 23-NOV-2000.
 PD 17-MAY-2000; 2000WO-US13576.
 PF 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX (CONJ-) CONJUCHEM INC.
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT -
 XX Disclosure; Page 498; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 52 AA;
 Query Match 43.2%; Score 283; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.5e-26;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 74 YRQSMNFGRLSFGCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 125
 Db 1 YRQSMNFGRLSFGCRGCTGVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 52

RESULT 13
 AAE09818
 ID AAE09818 standard; peptide; 52 AA.
 XX

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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:21 ; Search time 2.39401 Seconds
(without alignments)
646.939 Million cell updates/sec

Title: US-10-018-924-2_COPY_107_146
Perfect score: 219
Sequence: 1 SFGCRFGTCTGVGLAHQIYQFTDKDKDNVAPRSKISPOGY 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	219	100.0	185	1	ADML_HUMAN
2	213	97.3	188	1	ADML_PIG
3	208	95.0	188	1	ADML_CANFA
4	202	92.2	188	1	ADML_BOVIN
5	196	89.5	185	1	ADML_RAT
6	187	85.4	184	1	ADML_MOUSE
7	61	27.9	1541	1	MRP2_RAT
8	59	26.9	1545	1	MRP2_HUMAN
9	55	25.1	1564	1	MRP2_RABIT
10	54.5	24.9	436	1	SLS6_BRAOL
11	51	23.3	180	1	VG48_BPMU
12	51	23.3	1325	1	MRP4_HUMAN
13	50.5	23.1	459	1	G33_RAT
14	50.5	23.1	532	1	TYRO_RANNI
15	49.5	22.6	322	1	Y4KA_RHISN
16	49	22.4	435	1	SLS2_BRAOA
17	49	22.4	941	1	DNAB_RHOMR
18	49	22.4	1527	1	MRP3_HUMAN
19	48.5	22.1	465	1	INXB_CAEEL
20	48.5	22.1	960	1	L136_CAEEL
21	48	21.9	328	1	Z1PA_YERPE
22	48	21.9	396	1	PPAS_XENLA
23	48	21.9	425	1	SYH_METTH
24	48	21.9	496	1	NMT1_HUMAN
25	48	21.9	496	1	NMT1_MOUSE
26	48	21.9	497	1	NMT1_BOVIN
27	48	21.9	672	1	KPCA_BOVIN
28	48	21.9	672	1	KPCA_HUMAN
29	48	21.9	672	1	KPCA_MOUSE
30	48	21.9	672	1	KPCA_RABIT
31	48	21.9	672	1	KPCA_RAT
32	48	21.9	689	1	UVRPA_PSELE
33	48	21.9	1163	1	AT5C_HUMAN

ALIGNMENTS

RESULT 1	ADML_HUMAN	STANDARD;	PRT;	185 AA.
AC	P35318;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20			
DE	terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].			
GN	ADM OR AM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pheochromocytoma;			
RX	MEDLINE=93343928; PubMed=7688224;			
RA	Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;			
RT	"Cloning and characterization of cDNA encoding a precursor for human			
RT	adrenomedullin.";			
RL	Biochem. Biophys. Res. Commun. 194:720-725(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=94354869; PubMed=8074714;			
RA	Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuo H.,			
RA	Kitamura K., Eto T., Matsuo H.;			
RT	"Genomic structure of human adrenomedullin gene.";			
RL	Biochem. Biophys. Res. Commun. 203:631-639(1994).			
RN	[3]			
RP	SEQUENCE OF 95-146.			
RC	TISSUE=Pheochromocytoma;			
RX	MEDLINE=93249425; PubMed=8387282;			
RA	Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,			
RA	Matsuo H., Eto T.;			
RT	"Adrenomedullin: a novel hypotensive peptide isolated from human			
RT	pheochromocytoma.";			
RL	Biochem. Biophys. Res. Commun. 192:553-560(1993).			
RN	[4]			
RP	REVIEW.			
RX	MEDLINE=98240137; PubMed=9578982;			
RA	Samson W.K.;			
RT	"Proadrenomedullin-derived peptides.";			
RL	Front. Neuroendocrinol. 19:100-127(1998).			
RN	[5]			
RP	REVIEW.			
RX	MEDLINE=20053666; PubMed=10588445;			
RA	Champion H.C., Nussdorfer G.G., Kadowitz P.J.;			
RT	"Structure-activity relationships of adrenomedullin in the circulation			
RT	and adrenal gland.";			
RL	Regul. Pept. 85:1-8(1999).			
CC	-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR			
CC	AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE			
CC	PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE			
CC	KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP			

P56869 chlamydia m
Q929a0 chlamydia p
O84317 chlamydia t
Q00341 homo sapien
P38808 saccharomyc
Q24317 drosophila
Q08410 coturnix co
Q9f415 mycobacteri
P57175 buchnera ap
P53049 saccharomyc
P16144 homo sapien
O07815 neisseria m

34 48 21.9 1252 1 RPOB_CHLMU
35 48 21.9 1252 1 RPOB_CHLPN
36 48 21.9 1252 1 RPOB_CHLTR
37 48 21.9 1268 1 VGLN_HUMAN
38 47.5 21.7 144 1 YHP5_YEAST
39 47.5 21.7 438 1 PRT1_DROME
40 47 21.5 273 1 TYRO_COTJA
41 47 21.5 423 1 RECA_MYCFV
42 47 21.5 545 1 FLIF_BUCAI
43 47 21.5 1477 1 YORI_YEAST
44 47 21.5 1822 1 ITB4_HUMAN
45 46.5 21.2 76 1 RS18_NEIMA

defective in Eisai hyperbilirubinemic rats (EHBR).";
Int. Hepatol. Commun. 292:292-299(1996).
-1- FUNCTION: MEDIATES HEPATOBIILIARY EXCRETION OF NUMEROUS ORGANIC ANIONS.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
-1- DISEASE: DEFECTS IN ABCG2 ARE A CAUSE OF HEREDITARY CONJUGATED HYPERBILIRUBINEMIA (EHBR).
-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.

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EMBL; L49379; AAC42087.1; -;
EMBL; X96393; CAA65257.1; -;
EMBL; D86086; BAA13016.1; -;
HSSP; P13569; 1NBD.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR001140; ABC_transporter_tmnm.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 26 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 27 47 1 (BY SIMILARITY).
FT DOMAIN 48 67 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 68 88 2 (BY SIMILARITY).
FT DOMAIN 89 92 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 93 113 3 (BY SIMILARITY).
FT DOMAIN 114 125 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 126 146 4 (BY SIMILARITY).
FT DOMAIN 147 164 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 165 185 5 (BY SIMILARITY).
FT DOMAIN 186 309 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 310 330 6 (BY SIMILARITY).
FT DOMAIN 331 356 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 357 377 7 (BY SIMILARITY).
FT DOMAIN 378 433 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 434 454 8 (BY SIMILARITY).
FT DOMAIN 455 457 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 458 478 9 (BY SIMILARITY).
FT DOMAIN 479 540 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 541 561 10 (BY SIMILARITY).
FT DOMAIN 562 583 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 584 604 11 (BY SIMILARITY).
FT DOMAIN 605 967 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 968 988 12 (BY SIMILARITY).
FT DOMAIN 989 1029 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1030 1050 13 (BY SIMILARITY).
FT DOMAIN 1051 1093 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 1094 1114 14 (BY SIMILARITY).
FT DOMAIN 1115 1115 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1116 1136 15 (BY SIMILARITY).
FT DOMAIN 1137 1207 CYTOPLASMIC (BY SIMILARITY).
FT TRANSMEM 1208 1228 16 (BY SIMILARITY).
FT DOMAIN 1229 1230 EXTRACELLULAR (BY SIMILARITY).
FT TRANSMEM 1231 1251 17 (BY SIMILARITY).
FT DOMAIN 1252 1541 CYTOPLASMIC (BY SIMILARITY).
FT NP_BIND 667 674 ATP (POTENTIAL).
FT NP_BIND 1330 1337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1007 1007 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1010 1010 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1011 1011 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 420 M -> V (IN REF. 3).

SQ SEQUENCE 1541 AA; 173383 MW; D5FB55571BFDD39 CRC64;
Query Match 27.9%; Score 61; DB 1; Length 1541;
Best Local Similarity 38.2%; Pred. No. 2.2;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY 6 FGCTCTVQKLAHQIYQFTDKDKNDVAPRSKISPOG 39
Db 1479 FSQCTVTITTAHLRHITMSDKINVLNDNGKIVEYG 1512

RESULT 8
MRP2_HUMAN
ID MRP2_HUMAN STANDARD; PRT: 1545 AA.
AC Q92867; Q99663; Q92798; Q14022; Q92500; Q90MS2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance protein).
GN ABCG2 OR CMOAT1 OR CMOAT OR MRP2 OR CMRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96390592; PubMed=8797578;
RA Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M., Kagotani K., Okumura K., Akiyama S., Kuwano M.;
RT "A human canalicular multispecific organic anion transporter (cMOAT) gene is overexpressed in cisplatin-resistant human cancer cell lines with decreased drug accumulation.";
RL Cancer Res. 56:4124-4129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J., Baas F., Borst P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96279006; PubMed=8662992;
RA Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T., Keppler D.;
RT "cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance protein, cmrp, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats.";
RL J. Biol. Chem. 271:15091-15098(1996).
RN [4]
RP REVISIONS.
RA Keppler D.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99395001; PubMed=10464142;
RA Tsujii H., Koenig J., Rost D., Stoeckel B., Leuschner U., Keppler D.;
RT "Exon-intron organization of the human multidrug-resistance protein 2 (MRP2) gene mutated in Dubin-Johnson syndrome.";
RL Gastroenterology 117:653-660(1999).
RN [6]
RP VARIANT DJS TRP-768.
RX MEDLINE=98087571; PubMed=9425227;
RA Wada M., Foh S., Taniguchi K., Nakamura T., Uchiyama T., Kohno K., Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;
RT "Mutations in the canalicular multispecific organic anion transporter (cMOAT) gene, a novel ABC transporter, in patients with hyperbilirubinemia II/Dubin-Johnson syndrome.";
RL Hum. Mol. Genet. 7:203-207(1998).
RN [7]
RP VARIANTS DJS TRP-768 AND ARG-1382.
RX MEDLINE=99162196; PubMed=10053008;
RA Toh S., Wada M., Uchiyama T., Inokuchi A., Makino Y., Horie Y.,

RA Adachi Y., Sakisaka S., Kuwano M.;
 RT "Genomic structure of the canalicular multispecific organic anion-
 RT transporter gene (MRP2/cMOAT) and mutations in the ATP-binding-
 RT cassette region in Dubin-Johnson syndrome.";
 CC An. J. Hum. Genet. 64:739-746(1999).
 CC -1- FUNCTION: MEDIATES HEPATOBIILIARY EXCRETION OF NUMEROUS ORGANIC
 CC ANIONS. MAY FUNCTION AS A CELLULAR CISPLATIN TRANSPORTER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
 CC -1- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF DUBIN-JOHNSON SYNDROME
 CC (DJS), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY CONJUGATED
 CC HYPERBILIRUBINEMIA, AN INCREASE IN THE URINARY EXCRETION OF
 CC COPROPORPHYRIN ISOMER I, DEPOSITION OF MELANIN-LIKE PIGMENT IN
 CC HEPATOCYTES, AND PROLONGED RETENTION OF SULFOBROMOPHTHALEIN, BUT
 CC OTHERWISE NORMAL LIVER FUNCTION.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
 CC
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 CC
 CC EMBL; U63970; AAB39892.1; -;
 CC EMBL; U49248; AAB09422.1; -;
 CC EMBL; X96395; CAA65259.2; -;
 CC EMBL; AJ132244; CAB45309.1; JOINED.
 CC EMBL; AJ132287; CAB45309.1; JOINED.
 CC EMBL; AJ245625; CAB45309.1; JOINED.
 CC EMBL; AJ132288; CAB45309.1; JOINED.
 CC EMBL; AJ132289; CAB45309.1; JOINED.
 CC EMBL; AJ132290; CAB45309.1; JOINED.
 CC EMBL; AJ132291; CAB45309.1; JOINED.
 CC EMBL; AJ132292; CAB45309.1; JOINED.
 CC EMBL; AJ132293; CAB45309.1; JOINED.
 CC EMBL; AJ132294; CAB45309.1; JOINED.
 CC EMBL; AJ132295; CAB45309.1; JOINED.
 CC EMBL; AJ132296; CAB45309.1; JOINED.
 CC EMBL; AJ132297; CAB45309.1; JOINED.
 CC EMBL; AJ132298; CAB45309.1; JOINED.
 CC EMBL; AJ132299; CAB45309.1; JOINED.
 CC EMBL; AJ132300; CAB45309.1; JOINED.
 CC EMBL; AJ132301; CAB45309.1; JOINED.
 CC EMBL; AJ132302; CAB45309.1; JOINED.
 CC EMBL; AJ132303; CAB45309.1; JOINED.
 CC EMBL; AJ245626; CAB45309.1; JOINED.
 CC EMBL; AJ132304; CAB45309.1; JOINED.
 CC EMBL; AJ132305; CAB45309.1; JOINED.
 CC EMBL; AJ132306; CAB45309.1; JOINED.
 CC EMBL; AJ132307; CAB45309.1; JOINED.
 CC EMBL; AJ132308; CAB45309.1; JOINED.
 CC EMBL; AJ245627; CAB45309.1; JOINED.
 CC EMBL; AJ132309; CAB45309.1; JOINED.
 CC EMBL; AJ132310; CAB45309.1; JOINED.
 CC EMBL; AJ132311; CAB45309.1; JOINED.
 CC EMBL; AJ132312; CAB45309.1; JOINED.
 CC EMBL; AJ132313; CAB45309.1; JOINED.
 CC EMBL; AJ132314; CAB45309.1; JOINED.
 CC HSSP; P13569; INBD.
 CC MIM; 237500; -;
 CC InterPro; IPR003593; AAA.
 CC InterPro; IPR001140; ABC_transporter_tmemb.
 CC InterPro; IPR003439; ABC_transporter.
 CC InterPro; IPR001687; ATP_GTP_A.
 CC Pfam; PF00664; ABC_membrane; 2.
 CC Pfam; PF00005; ABC_tran; 2.
 CC SMART; SM00382; AAA; 1.
 CC PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat; Disease mutation.

FT DOMAIN 1 27
 FT TRANSMEM 28 48
 FT DOMAIN 49 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 93
 FT TRANSMEM 94 114
 FT DOMAIN 115 126
 FT TRANSMEM 127 147
 FT DOMAIN 148 165
 FT TRANSMEM 166 186
 FT DOMAIN 187 333
 FT TRANSMEM 314 334
 FT DOMAIN 335 360
 FT TRANSMEM 361 381
 FT DOMAIN 382 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 461
 FT TRANSMEM 462 482
 FT DOMAIN 483 544
 FT TRANSMEM 545 565
 FT DOMAIN 566 588
 FT TRANSMEM 588 608
 FT DOMAIN 609 671
 FT TRANSMEM 671 678
 FT NP_BIND 671 678
 FT NP_BIND 1334 1341
 FT CARBOHYD 7 7
 FT CARBOHYD 12 12
 FT CARBOHYD 1011 1011
 FT VARIANT 768 768
 FT VARIANT 1382 1382
 FT CONFLICT 1188 1188
 FT CONFLICT 1430 1430
 FT CONFLICT 1515 1515
 FT SEQUENCE 1545 AA; 174190 MW; EA12668A4DD0F391 CRC64;
 Query Match 26.9%; Score 59; DB 1; Length 1545;
 Best Local Similarity 37.8%; Pred. No. 4.2;
 Matches 14; Conservative 5; Mismatches 14; Indels 4; Gaps 1;
 QY 6 FGCTCTVOKLAHQIYQFTDKDKDNVAPRSKI----SPQ 38
 Db 1483 FAHCTVTITIAHRLTIWDSKVDKGVLDNGKIIECGSPE 1519
 RESULT 9
 MRP2_RABIT STANDARD; PRT; 1564 AA.
 ID MRP2_RABIT
 AC Q28689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Canalicular multispecific organic anion transporter 1 (Multidrug
 DE resistance-associated protein 2) (Canalicular multidrug resistance
 DE protein) (Epithelial basolateral chloride conductance regulator).
 GN ABCC2 OR MRP2 OR EBCR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_taxid=9986;


```
DR InterPro: IPR000858; Slocus_glycop.
DR Pfam: PF01453; Agglutinin; 1.
DR Pfam: PF00954; Slocus_glycop; 1.
DR SMART: SM00108; Blectin; 1.
DR SMART: SM00473; PAN_AP; 1.
KW Self-Incompatibility; Glycoprotein; Polymorphism; Signal.
FT SIGNAL 1 31
FT CHAIN 32 436
FT CARBOHYD 46 46
FT CARBOHYD 64 64
FT CARBOHYD 114 114
FT CARBOHYD 121 121
FT CARBOHYD 125 125
FT CARBOHYD 245 245
FT CARBOHYD 261 261
FT CARBOHYD 390 390
FT CARBOHYD 436 436
SQ SEQUENCE 436 AA; 49779 MW; E3326358885A515 CRC64;

Query Match 24.9%; Score 54.5; DB 1; Length 436;
Best Local Similarity 28.6%; Pred. NO. 4.8;
Matches 14; Conservative 10; Mismatches 14; Indels 11; Gaps 2;

QY 3 GCRF-GTCTVQKLAHQIYQFTDKDKD-----NVAPRSKISPGY 40
DB 227 GVRFGIPEDOKLSYMYNFTENSEVAYFRMTWNSIYSLTSLSEGY 275

RESULT 11
VG48_BPMU STANDARD; PRT; 180 AA.
AC QG48_BPMU
ID QG48_BPMU
RT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein gp48.
GN 48.
OS Bacteriophage Mu.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=10677;
RN [1]
RP Morgan G., Hatfull G., Hendrix R.;
RA "Genome of Bacteriophage Mu and comparison with the Haemophilus
RT Influenzae Mu-like prophage Flumu.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO H. INFLUENZAE H11521 AND SOME, TO E. COLI YMFO.
CC -----
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CC -----
DR EMBL: AF083977; AAF01126.1; -.
SQ SEQUENCE 180 AA; 20468 MW; 3045A6C185B48BF9 CRC64;

Query Match 23.3%; Score 51; DB 1; Length 180;
Best Local Similarity 50.0%; Pred. NO. 5.8;
Matches 11; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 9 CTVQKLA-AHQIYQFTDKDKDN 28
DB 159 CLEKYPKPAHQIYKFVYHGDGN 180

RESULT 12
MRP4_HUMAN STANDARD; PRT; 1325 AA.
ID MRP4_HUMAN
AC O15439; Q9Y6J2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance-associated protein 4 (MRP/CMOAT-related ABC
DE transporter) (MOAT-B).
DE ABC4 OR MRP4.
DE Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DE NCBI_TaxID=9606;
DE [1]
DE SEQUENCE FROM N.A.
DE MEDLINE=98324262; PubMed=9661885;
DE Lee K., Belinsky M.G., Bell D.W., Testa J.R., Kruh G.D.;
DE "Isolation of MOAT-B, a widely expressed multidrug resistance-
DE associated protein/canicular multispecific organic anion
DE transporter-related transporter.";
DE Cancer Res. 58:2741-2747(1998).
DE [2]
DE SEQUENCE OF 1155-1316 FROM N.A.
DE TISSUE=Brain;
DE MEDLINE=97413640; PubMed=9270026;
DE Kool M., de Haas M., Scheffer G.L., Scheper R.J., van Eijk M.J.,
DE Julin J.A., Baas F., Borst P.;
DE "Analysis of expression of cMOAT (MRP2), MRP3, MRP4, and MRP5,
DE homologues of the multidrug resistance-associated protein gene
DE (MRP1), in human cancer cell lines.";
DE Cancer Res. 57:3537-3547(1997).
DE -!- FUNCTION: MAY BE AN ORGANIC ANION PUMP RELEVANT TO CELLULAR
DE DETOXIFICATION.
DE -!- SUBCELLULAR LOCATION: Integral membrane protein.
DE -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH PARTICULARLY HIGH
DE LEVELS IN PROSTATE, BUT IS BARELY DETECTABLE IN LIVER.
DE -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
DE -----
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DE -----
DE EMBL: AF071202; AAC27076.1; -.
DE EMBL: U83660; AAB71757.1; -.
DE HSP; P13569; INHD.
DE MIM; 605250; -.
DE InterPro: IPR003593; AAA.
DE InterPro: IPR003439; ABC_transportr.
DE InterPro: IPR001687; ATP_GTP_A.
DE Pfam: PF00005; ABC_tran; 2.
DE Pfam: PF00664; ABC_membrane; 2.
DE SMART: SM00382; AAA; 2.
DE PROSITE: PS00211; ABC_TRANSPORTER; 2.
DE ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
DE TRANSMEM 93 113 POTENTIAL.
DE TRANSMEM 136 156 POTENTIAL.
DE TRANSMEM 207 227 POTENTIAL.
DE TRANSMEM 228 248 POTENTIAL.
DE TRANSMEM 328 348 POTENTIAL.
DE TRANSMEM 351 371 POTENTIAL.
DE TRANSMEM 440 460 POTENTIAL.
DE TRANSMEM 710 730 POTENTIAL.
DE TRANSMEM 771 791 POTENTIAL.
DE TRANSMEM 836 856 POTENTIAL.
DE TRANSMEM 858 878 POTENTIAL.
DE TRANSMEM 954 974 POTENTIAL.
DE TRANSMEM 977 997 POTENTIAL.
DE TRANSMEM 1038 1058 POTENTIAL.
DE NP_BIND 445 452 ATP (POTENTIAL).
DE NP_BIND 1075 1082 ATP (POTENTIAL).
DE CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
DE CARBOHYD 690 690 N-LINKED (GLCNAC. . .) (POTENTIAL).
DE CARBOHYD 746 746 N-LINKED (GLCNAC. . .) (POTENTIAL).
DE CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
DE CARBOHYD 792 792 N-LINKED (GLCNAC. . .) (POTENTIAL).
```



```
FT CARBOHYD 1176 1176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1309 1309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1302 1302 H -> D (IN REF. 2).
SQ SEQUENCE 1325 AA; 149539 MW; 9C5750A748BB96CE CRC64;

Query Match
Best Local Similarity 40.9%; Pred. No. 46;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 5 RFGCTVQKLAHQIYQFTDKDK 26
Db 1222 KFAHCTVLTIAHRLNTIIDS 1243

RESULT 13
G33_RAT
ID G33_RAT STANDARD; PRT; 459 AA.
AC P05432;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Gene 33 polypeptide.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=89385990; PubMed=2780291;
RA Chrapkiewicz N.B., Davis C.M., Chu D.T.W., Granner D.K.;
RT "Rat gene 33: analysis of its structure, messenger RNA and basal
promoter activity.";
RL Nucleic Acids Res. 17:6651-6667(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=89138017; PubMed=3224831;
RA Tindal M.H., Lee K.L., Isham K.R., Cadilla C., Kenney F.T.;
RT "Structure of a multihormonally regulated rat gene.";
RL Gene 71:413-420(1988).
CC -1- INDUCTION: BY CAMP, GLUCOCORTICOIDS, PHORBOL ESTERS AND
INSULIN.
CC
CC
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CC
DR EMBL; X07266; CAA30252.1; -
DR EMBL; M23572; AAB08828.1; -
DR EMBL; M23570; AAB08828.1; JOINED.
DR EMBL; M23571; AAB08828.1; JOINED.
DR PIR; S03116; S03116.
SQ SEQUENCE 459 AA; 49941 MW; EBD90F1175AC549 CRC64;

Query Match
Best Local Similarity 23.1%; Score 50.5; DB 1; Length 459;
Matches 11; Conservative 6; Mismatches 12; Indels 5; Gaps 1;

QY 5 RFGCTVQKLAHQIYQFTDKDNVAPRSKISQ 38
Db 262 RISSCT-----HRASPSDEKPEIPRPVPIPR 290

RESULT 14
TYRO_RANNI
ID TYRO_RANNI STANDARD; PRT; 532 AA.
AC Q04604;
DT 01-OCT-1993 (Rel. 27, Created)
```

```
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
GN TYR OR TYRS.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077054; PubMed=1446833;
RA Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.;
RT "Cloning and sequencing of the cDNA encoding tyrosinase of the
Japanese pond frog, Rana nigromaculata.";
RL Gene 121:359-363(1992).
RN [2]
RP SEQUENCE OF 1-277 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95290234; PubMed=7772385;
RA Miura I., Okumoto H., Makino K., Nakata A., Nishioka M.;
RT "Analysis of the tyrosinase gene of the Japanese pond frog, Rana
nigromaculata: cloning and nucleotide sequence of the genomic DNA
containing the tyrosinase gene and its flanking regions.";
RL Jpn. J. Genet. 70:79-82(1995).
CC -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) -> L-DOPA +
DOPAquinone + H(2)O.
CC -1- COFACTOR: BINDS TWO COPPER IONS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
CC
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CC
DR EMBL; D12514; BAA02077.1; -
DR EMBL; D37779; BAA07034.1; -
DR PIR; JCI392; JCI392.
DR InterPro: IPR002227; Tyrosinase.
DR Pfam: PF00264; tyrosinase.1.
DR PRINTS; PR00092; TYROSINASE.
DR PROSITE; PS00497; TYROSINASE_1; 1.
DR PROSITE; PS00498; TYROSINASE_2; 1.
KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
KW Transmembrane; Melanin biosynthesis.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 532 TYROSINASE.
FT DOMAIN 20 475 LUMINAL, MELANOSOME (POTENTIAL).
FT TRANSMEM 476 499 POTENTIAL.
FT DOMAIN 500 532 CYTOPLASMIC (POTENTIAL).
FT METAL 184 184 COPPER A (BY SIMILARITY).
FT METAL 206 206 COPPER A (BY SIMILARITY).
FT METAL 215 215 COPPER A (BY SIMILARITY).
FT METAL 367 371 COPPER B (BY SIMILARITY).
FT METAL 371 371 COPPER B (BY SIMILARITY).
FT METAL 394 394 COPPER B (BY SIMILARITY).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 10 10 T -> A.
SQ SEQUENCE 532 AA; 60115 MW; B27D3080F0C74B3A CRC64;

Query Match
Best Local Similarity 23.1%; Score 50.5; DB 1; Length 532;
Query Match
Best Local Similarity 34.8%; Pred. No. 21;
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 ; Search time 4.58853 Seconds
(without alignments)
837.648 Million cell updates/sec

Title: US-10-018-924-2_COPY_107_146

Perfect score: 219
Sequence: 1 SFGCRPGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGQY 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	100.0	185	JN0684	adrenomedullin pre
2	213	97.3	188	S41600	adrenomedullin - p
3	196	89.5	185	JN0766	adrenomedullin pre
4	61.5	28.1	430	T14536	S-locus-specific g
5	61	27.9	1341	S171839	canalicular multidi
6	59	26.9	1545	S171841	multidrug resistan
7	58.5	26.7	189	A99638	hypothetical prote
8	58.5	26.7	189	A85489	hypothetical prote
9	58.5	26.7	431	T14415	S-locus-specific g
10	55.5	25.3	428	T14529	S-locus-specific g
11	55	25.1	373	G84107	S-locus-specific g
12	54.5	24.9	428	T07814	S-locus-specific g
13	54.5	24.9	436	A27827	lipopolysaccharide
14	53.5	24.4	427	T14424	S-locus-specific g
15	53.5	24.4	428	T14423	S-locus-specific g
16	53	24.2	465	T15540	S-locus-specific g
17	52.5	24.0	428	T14416	hypothetical prote
18	52.5	24.0	428	T14530	S-locus-specific g
19	52.5	24.0	429	T07809	S-locus-specific g
20	51.5	23.5	426	T07810	S-receptor kinase
21	51.5	23.5	429	T14528	S-locus-specific g
22	51	23.3	93	E91004	S-locus-specific g
23	51	23.3	93	E85637	hypothetical prote
24	51	23.3	319	S20799	hypothetical prote
25	51	23.3	429	T14533	hypothetical prote
26	51	23.3	608	AD2000	S-locus-specific g
27	51	23.3	759	T16368	ABC transporter At
28	51	23.3	857	T14471	hypothetical prote
29	50.5	23.1	171	D70832	probable S-recepto
					hypothetical prote

hypothetical prote
gene 33 protein, h
monophenol monooxy
hypothetical prote
S-receptor kinase
S-receptor kinase
hypothetical prote
myb-related transc
hypothetical prote
exonuclease SbcC I
hypothetical prote
hypothetical prote
conserved hypotet
sugar phosphate nu
S-locus-specific g

ALIGNMENTS

RESULT 1

JN0684
adrenomedullin precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C:Accession: JC2351; JN0684; PN0548; JN0476
R: Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, K.; Eto, T.
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A:Title: Genomic structure of human adrenomedullin gene.
A:Reference number: JC2351; MUID:94354869
A:Accession: JC2351
A:Molecule type: DNA
A:Residues: 1-185 <ISH>
A:Cross-references: GB:S73906; NID:q765329; PIDN:AAC60642.1; PID:q765330
A:Experimental source: Pheochromocytoma
R: Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A:Reference number: JN0684; MUID:93343928
A:Accession: JN0684
A:Molecule type: mRNA
A:Residues: 1-185 <KIT>
A:Cross-references: GB:D14874; NID:q455470; PIDN:BAA03589.1; PID:q500612
A:Accession: PN0548
A:Molecule type: protein
R: Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A:Reference number: JN0476; MUID:93249425
A:Accession: JN0476
A:Molecule type: protein
A:Residues: 95-146 <KIT>
A:Experimental source: pheochromocytoma
C:Genetics:
A:Gene: GDB:ADM
A:Cross-references: GDB:217070; OMIM:103275
A:Map position: l1pter-11qter
A:Introns: 33/2; 83/2
C:Keywords: amidated carboxyl end; blood pressure control; hormone
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:95-146/Product: adrenomedullin #status experimental <MAT>
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:110-115/Disulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 100.0%; Score 219; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 40
|||||
Db 107 SFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 2

S41600
adrenomedullin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S41600
R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A:Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding
A:Reference number: S41600; MUID:94139945
A:Accession: S41600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-188 <KIT>
A:Cross-references: GB:D14875; NID:9439721; PIDN:BAA03590.1; PID:9496379

Query Match 97.3%; Score 213; DB 2; Length 188;
Best Local Similarity 97.5%; Pred. No. 6.1e-22;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 40
|||||
Db 107 SFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 3

JN0766
adrenomedullin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C:Accession: JN0766; PN0610
R:Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, H.; Eto, T.
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A:Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensive
A:Reference number: JN0766; MUID:93384621
A:Accession: JN0766
A:Molecule type: mRNA
A:Residues: 1-185 <SAK>
A:Accession: PN0610
A:Molecule type: protein
A:Residues: 22-41 <SA>
C:Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedullin.

C:Keywords: amidated carboxyl end
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:94-143/Product: adrenomedullin #status predicted <MA>
F:141/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 89.5%; Score 196; DB 2; Length 185;
Best Local Similarity 87.5%; Pred. No. 1.4e-19;
Matches 35; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SFGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 40
|||||
Db 104 STGCRFGCTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 143

RESULT 4

Tl4536
S-locus-specific glycoprotein - wild cabbage (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica oleracea (wild cabbage)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: Tl4536

R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A:Title: Striking sequence similarity in inter- and intra-specific comparisons of a cl
echanism.
A:Reference number: Z18078; MUID:97352858
A:Accession: Tl4536
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-430 <KUS>
A:Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 28.1%; Score 61.5; DB 2; Length 430;
Best Local Similarity 28.6%; Pred. No. 1.4;
Matches 14; Conservative 12; Mismatches 12; Indels 11; Gaps 2;

QY 3 GCRF-GTCTVOKLAHQIYQFTDKDKD-----NVAPRSKISPOGY 40
|||||
Db 220 GIRSGIPEDKLSYMYNFETENNEVAYTRMTNNSIYRLTVSPGY 268

RESULT 5

S71839
canalicular multidrug resistance protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C:Accession: S71839
R:Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, J.
J. Biol. Chem. 271, 15091-15098, 1996
A:Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance
A:Reference number: S71839; MUID:96279006
A:Accession: S71839
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1541 <RUE>
A:Cross-references: EMBL:X96393; NID:g1292881; PIDN:CAA65257.1; PID:g1617207
C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homolo
C:Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F:100-124/Domain: transmembrane #status predicted <TM01>
F:127-151/Domain: transmembrane #status predicted <TM02>
F:160-187/Domain: transmembrane #status predicted <TM03>
F:305-329/Domain: transmembrane #status predicted <TM04>
F:334-381/Domain: transmembrane #status predicted <TM05>
F:431-451/Domain: transmembrane #status predicted <TM06>
F:456-476/Domain: transmembrane #status predicted <TM07>
F:536-564/Domain: transmembrane #status predicted <TM08>
F:574-602/Domain: transmembrane #status predicted <TM09>
F:650-833/Domain: ATP-binding cassette homology <ABC1>
F:667-674/Region: nucleotide-binding motif A (P-loop)
F:966-994/Domain: transmembrane #status predicted <TM10>
F:1018-1046/Domain: transmembrane #status predicted <TM11>
F:1104-1132/Domain: transmembrane #status predicted <TM12>
F:1203-1228/Domain: transmembrane #status predicted <TM13>
F:1313-1506/Domain: ATP-binding cassette homology <ABC2>
F:1330-1337/Region: nucleotide-binding motif A (P-loop)
F:6, 1007, 1010, 1011/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 27.9%; Score 61; DB 1; Length 1541;
Best Local Similarity 38.2%; Pred. No. 6.2;
Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 6 FGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPOG 39
|||||
Db 1479 FSQCTVITIAHRLHTIMDSKIMVLDNGKIVEYG 1512

RESULT 6

S71841
multidrug resistance protein, canalicular - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C:Accession: S71841; S71840

Nature 326, 617-619, 1987

A>Title: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus
A:Reference number: A93392
A:Accession: A27827
A:Molecule type: mRNA
A:Residues: 1-436 <NAS>
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein
F:1-31/domain: signal sequence #status predicted <SIG>
F:32-436/Product: S-locus-specific glycoprotein S6 #status predicted <MAT>
F:40-434/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match 24.9%; Score 54.5; DB 2; Length 436;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 14; Conservative 10; Mismatches 14; Indels 11; Gaps 2;

QY 3 GCRR-GTCTVQKLAHQIYFTDKD-----NVAPRSKISPGY 40
| | | : | | : | | : | | : | | : | | :
Db 227 GVRFSGIPEDQKLVMYNFTENSEEVAYTFRTNNISYRLTLSEGY 275

RESULT 14

Tl4424

S-locus-specific glycoprotein - turnip (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica rapa (turnip)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: Tl4424
R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A>Title: Striking sequence similarity in inter- and intra-specific comparisons of c f l
echanism.
A:Reference number: Z18078; MUID:97352858
A:Accession: Tl4424
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-427 <KUS>
A:Cross-references: EMBL:D85225; NID:g2351181; PIDN:BAA21959.1; PID:g2351178
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 24.4%; Score 53.5; DB 2; Length 427;
Best Local Similarity 28.6%; Pred. No. 18;
Matches 14; Conservative 10; Mismatches 14; Indels 11; Gaps 2;

QY 3 GCRR-GTCTVQKLAHQIYFTDKD-----NVAPRSKISPGY 40
| | | : | | : | | : | | : | | : | | :
Db 220 GVRFGIPEDQKLNTVMYNFTENSEEVAYTFRTNNISYRKLSSEG 268

RESULT 15

Tl4423

S-locus-specific glycoprotein - turnip (fragment)
N:Alternate names: S glycoprotein
C:Species: Brassica rapa (turnip)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C:Accession: Tl4423
R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A>Title: Striking sequence similarity in inter- and intra-specific comparisons of c f l
echanism.
A:Reference number: Z18078; MUID:97352858
A:Accession: Tl4423
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-428 <KUS>
A:Cross-references: EMBL:D85223; NID:g2351177; PIDN:BAA21957.1; PID:g2351178
C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C:Keywords: glycoprotein

Query Match 24.4%; Score 53.5; DB 2; Length 428;
Best Local Similarity 28.6%; Pred. No. 18;
Matches 14; Conservative 10; Mismatches 14; Indels 11; Gaps 2;

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Job time : 7.58853 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 14:45:20 ; Search time 9 67581 Seconds
(without alignments)
459.181 Million cell updates/sec

Title: US-10-018-924-2_COPY_107_146

Perfect score: 219

Sequence: 1 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	100.0	52	22 AAB75110	Human adrenomedullin
2	219	100.0	52	22 AAB91759	Adrenomedullin pep
3	219	100.0	52	22 AAE09818	Human adrenomedullin
4	219	100.0	53	22 AAB75111	Glycine extended h
5	219	100.0	53	22 AAB75112	Glycine extended a
6	219	100.0	62	22 AAB75113	Linker peptide-adr
7	219	100.0	120	22 AAB75122	uspa(1-57)-(A)-(GS
8	219	100.0	120	22 AAB75123	uspa(1-56)-(DD)-(GS
9	219	100.0	147	22 AAB75124	uspa(1-84)-(A)-(GS
10	219	100.0	170	22 AAB75114	Thioredoxin-(GSGSG
11	219	100.0	185	22 AAB49697	Human adrenomedullin

12	219	100.0	185	22 AAB60344	Human adrenomedullin
13	213	97.3	188	22 AAB49698	Porcine adrenomedu
14	213	97.3	188	22 AAB60345	Porcine adrenomedu
15	196	89.5	40	22 AAB91768	Adrenomedullin pep
16	196	89.5	50	22 AAE09819	Rat adrenomedullin
17	196	89.5	185	22 AAB49699	Rat adrenomedullin
18	196	89.5	185	22 AAB60346	Rat adrenomedullin
19	184.5	84.2	53	22 AAB91767	Rat adrenomedullin
20	181.5	82.9	37	22 AAB91761	Adrenomedullin pep
21	179.5	82.0	52	22 AAB91765	Adrenomedullin pep
22	163	74.4	31	18 AAW25160	Human preproadreno
23	163	74.4	31	22 AAB91762	Adrenomedullin pep
24	163	74.4	31	22 AAE09827	Human adrenomedullin
25	61	27.9	1541	18 AAW33361	Rat canaliculic mu
26	60	27.4	231	21 AAB11449	Human cMOAT C-term
27	60	27.4	231	21 AAB28224	Multi-drug resista
28	60	27.4	1545	18 AAW33362	Human canaliculic
29	59	26.9	1545	19 AAW55966	Human canaliculic
30	57	26.0	13	18 AAW25159	Human preproadreno
31	56	25.6	1302	22 ABB65954	Drosophila melanog
32	55	25.1	1344	22 ABB59224	Drosophila melanog
33	54	24.7	1327	22 ABB63391	Drosophila melanog
34	54	24.7	1346	22 ABB65953	Drosophila melanog
35	53.5	24.4	436	19 AAW56306	Clas I S-locus gly
36	53.5	24.4	845	19 AAW56307	Clas I S-receptor
37	53	24.2	892	22 ABB62270	Drosophila melanog
38	53	24.2	1348	22 ABB60761	Drosophila melanog
39	52	23.7	229	22 ABB05415	Novel human diagno
40	52	23.7	229	22 ABB13273	Novel human diagno
41	52	23.7	677	22 ABB09129	Novel human diagno
42	52	23.7	775	19 AAW58582	Kojibiose phosphor
43	52	23.7	939	22 ABB14932	Novel human diagno
44	52	23.7	994	22 ABB10411	Novel human diagno
45	52	23.7	1547	22 ABB66152	Drosophila melanog

ALIGNMENTS

RESULT 1

AAB75110

ID AAB75110 standard; Protein; 52 AA.

XX AAB75110;

XX 31-JUL-2001 (first entry)

XX Human adrenomedullin (AM) protein.

XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;

XX Adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.

XX Homo sapiens.

XX WO200127310-A1.

XX 19-APR-2001.

XX 10-OCT-2000; 2000WO-JP07023.

XX 15-OCT-1999; 99JP-0294147.

XX (SHIO) SHIONOGI & CO LTD.

XX Takimoto A, Mitsuda Y, Nakayama T, Mitsuhashi K;

XX WPI; 2001-282044/29.

XX N-PSDB; AAB19806.

XX Producing adrenomedullin useful for pharmaceutical and diagnostic

XX PT application comprises producing fused adrenomedullin precursor using a

XX recombinant host

XX

PS Disclosure; Page 45; 75pp; Japanese.

XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.

XX Sequence 52 AA;
SQ Query Match 100.0%; Score 219; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
DB 13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 2
AAB91759
ID AAB91759 standard; Peptide; 52 AA.

XX AAB91759;

XX 22-JUN-2001 (first entry)

XX Adrenomedullin peptide (AM) SEQ ID NO:935.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

XX Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 498; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 52 AA;

XX Query Match 100.0%; Score 219; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
DB 13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 3
AAE09818
ID AAE09818 standard; peptide; 52 AA.

XX AAE09818;

XX 29-NOV-2001 (first entry)

XX Human adrenomedullin peptide #1.

XX Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW CGRP-receptor identification; adrenomedullin.

XX Homo sapiens.

XX US6268474-B1.

XX 31-JUL-2001.

XX 30-APR-1998; 98US-0070504.

XX 30-APR-1998; 98US-0070504.

XX (UYCR-) UNIV CREIGHTON.

XX Smith DD, Saha S, Abel PW;

XX WPI; 2001-564216/63.

XX Vasoactive peptides useful for inhibiting calcitonin gene related
PT peptide receptor activity -

XX Claim 5; Column 25-26; 24pp; English.

XX The invention relates to antagonists of the vasoactive peptide
CC calcitonin gene related peptide (CGRP) and other members of the
CC CGRP superfamily. The invention also relates to amino the terminal
CC modifications of peptides to improve their ability to bind to a
CC member of the CGRP-receptor super-family. CGRP antagonists are
CC used for inhibiting CGRP activity which can be used in vitro e.g.
CC in assays to identify and/or isolate CGRP receptors or with intact
CC cells either in vitro or in vivo to inhibit the effect of CGRP
CC binding to its receptor. The present sequence is human
CC adrenomedullin peptide.

XX Sequence 52 AA;

XX Query Match 100.0%; Score 219; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
DB 13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52

```

RESULT 4
AAB75111
ID AAB75111 standard; Protein; 53 AA.
XX
AC AAB75111;
XX
DT 31-JUL-2001 (first entry)
XX
DE Glycine extended human adrenomedullin (AM-gly) protein.
XX
DE Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP07023.
XX
PR 15-OCT-1999; 99JP-0294147.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR WPI; 2001-282044/29.
XX
DR N-PSDB; AAH19807.
XX
PT Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host
XX
PS Example 1; Page 46; 75pp; Japanese.
XX
CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 53 AA;

Query Match 100.0%; Score 219; DB 22; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGCTGVOKLAHQIYQFTDKDNVAPRSKISPOGY 40
Db 13 SFGCRFGCTGVOKLAHQIYQFTDKDNVAPRSKISPOGY 52

RESULT 5
AAB75112
ID AAB75112 standard; Protein; 53 AA.
XX
AC AAB75112;
XX
DT 31-JUL-2001 (first entry)
XX
DE Glycine extended adrenomedullin (AM-gly) protein.
XX
DE Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
OS Synthetic.

```

```

XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP07023.
XX
PR 15-OCT-1999; 99JP-0294147.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR WPI; 2001-282044/29.
XX
DR N-PSDB; AAH19808.
XX
PT Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host
XX
PS Disclosure; Page 47; 75pp; Japanese.
XX
CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 53 AA;

Query Match 100.0%; Score 219; DB 22; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGCTGVOKLAHQIYQFTDKDNVAPRSKISPOGY 40
Db 13 SFGCRFGCTGVOKLAHQIYQFTDKDNVAPRSKISPOGY 52

RESULT 6
AAB75113
ID AAB75113 standard; Protein; 62 AA.
XX
AC AAB75113;
XX
DT 31-JUL-2001 (first entry)
XX
DE Linker peptide-adrenomedullin (AM) precursor protein.
XX
KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
OS Homo sapiens.
OS Synthetic.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP07023.
XX
PR 15-OCT-1999; 99JP-0294147.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR WPI; 2001-282044/29.
DR N-PSDB; AAH19809.

```

XX Producing adrenomedullin useful for pharmaceutical and diagnostic.
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX
XX
XX Claim 20; Page 48; 75pp; Japanese.
XX
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 62 AA;
Query Match 100.0%; Score 219; DB 22; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.1e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
Db 22 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 61
RESULT 7
AAB75122
ID AAB75122 standard; Protein; 120 AA.
XX
AC AAB75122;
XX
DT 31-JUL-2001 (first entry)
XX
DE UsPA(1-57)-(A)-(GSGGDAFE)-AM-gly protein.
XX
KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP07023.
XX
PR 15-OCT-1999; 99JP-0294147.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsuishima K;
XX
DR WPI; 2001-282044/29.
DR N-PSDB; AAH19864.
XX
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX
XX Claim 17; Page 68; 75pp; Japanese.
XX
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the

CC exemplification of the present invention.
XX
XX
SQ Sequence 120 AA;
Query Match 100.0%; Score 219; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
Db 80 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 119
RESULT 8
AAB75123
ID AAB75123 standard; Protein; 120 AA.
XX
AC AAB75123;
XX
DT 31-JUL-2001 (first entry)
XX
DE UsPA(1-56)-(DD)-(GSGGDAFE)-AM-gly protein.
XX
KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP07023.
XX
PR 15-OCT-1999; 99JP-0294147.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsuishima K;
XX
DR WPI; 2001-282044/29.
DR N-PSDB; AAH19865.
XX
XX Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX
XX Claim 17; Page 69-70; 75pp; Japanese.
XX
XX The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 120 AA;
Query Match 100.0%; Score 219; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
Db 80 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 119
RESULT 9
AAB75124

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ID XX AAB75124 standard; Protein; 147 AA.
XX AC AAB75124;
XX DT 31-JUL-2001 (first entry)
XX DE UspA(1-84)-(A)-(GSGGDAFE)-AM-gly protein.
XX KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
XX KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200127310-A1.
XX PD 19-APR-2001.
XX PF 10-OCT-2000; 2000WO-JP07023.
XX PR 15-OCT-1999; 99JP-0294147.
XX PS (SHIO ) SHIONOGI & CO LTD.
XX PA Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX PI WPI; 2001-282044/29.
XX DR N-PSDB; AAH19866.
XX DR Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX PS Claim 17; Page 71; 75pp; Japanese.
XX CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX SQ Sequence 147 AA;

Query Match 100.0%; Score 219; DB 22; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.3e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
Db 107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 10
AAB75114
ID AAB75114 standard; Protein; 170 AA.
XX AC AAB75114;
XX DT 31-JUL-2001 (first entry)
XX DE Thioedoxin-(GSGGDAFE)-AM-gly protein.
XX KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
XX KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200127310-A1.

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XX 19-APR-2001.
XX 10-OCT-2000; 2000WO-JP07023.
XX 15-OCT-1999; 99JP-0294147.
XX (SHIO ) SHIONOGI & CO LTD.
XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX WPI; 2001-282044/29.
XX DR N-PSDB; AAH19810.
XX DR Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host -
XX PS Claim 17; Page 49-50; 75pp; Japanese.
XX CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restriction digestion of the
CC fused protein by a protease followed by collection of sediment; and
CC (c) dissolving the sediment and extracting adrenomedullin precursor.
CC The method can be used for the production of adrenomedullin precursor
CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
CC and AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention.
XX SQ Sequence 170 AA;

Query Match 100.0%; Score 219; DB 22; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.8e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 40
Db 130 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPGY 169

RESULT 11
AAB49697
ID AAB49697 standard; Protein; 185 AA.
XX AC AAB49697;
XX DT 04-APR-2001 (first entry)
XX DE Human adrenomedullin amino acid sequence.
XX KW Passive elongation; vesicle smooth muscle; uropathic activity;
XX KW adrenomedullin; urinary disorder; incontinence; human.
XX OS Homo sapiens.
XX PN WO200078338-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-JP04166.
XX PR 23-JUN-1999; 99JP-0177549.
XX PS (SHIO ) SHIONOGI & CO LTD.
XX PA Yanagita T;
XX PI WPI; 2001-080754/09.
XX DR N-PSDB; AAF29138.
XX DR Composition for promoting passive elongation of vesicle smooth muscle
XX PT comprises adrenomedullin -
PT

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XX PS Claim 1; Page 26-27; 42pp; Japanese.

XX CC This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedullin, and has uterine contraction activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the human adrenomedullin protein, which is used in the composition of the invention.

XX SQ Sequence 185 AA;

Query Match 100.0%; Score 219; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 40
Db 107 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 146

RESULT 12
AAB60344
ID AAB60344 standard; Protein; 185 AA.
AC AAB60344;
XX DT 06-APR-2001 (first entry)
XX DE Human adrenomedullin precursor.
XX KW Human; adrenomedullin; precursor; bradykinin antagonist;
KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW dysmenorrhea; obstetric; gynaecological.
XX OS Homo sapiens.
XX PN WO200078339-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-JP04167.
XX PR 23-JUN-1999; 99JP-0177548.
XX PR 21-MAR-2000; 2000JP-0079171.
XX PA (SHIO) SHIONOGI & CO LTD.
XX PI Yanagita T;
XX DR WPI: 2001-080755/09.
XX DR N-PSDB; AAF27228.
XX CC Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin

XX PS Claim 7; Page 37-38; 54pp; Japanese.

XX CC The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhea. The present sequence represents human adrenomedullin precursor.

XX SQ Sequence 185 AA;

Query Match 100.0%; Score 219; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 40
Db 107 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 146

RESULT 13
AAB49698
ID AAB49698 standard; Protein; 188 AA.
XX AC AAB49698;
XX DT 04-APR-2001 (first entry)
XX DE Porcine adrenomedullin amino acid sequence.
XX KW Passive elongation; vesicle smooth muscle; uropathic activity;
KW adrenomedullin; urinary disorder; incontinence; proctine.
XX OS Sus scrofa.
XX PN WO200078338-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-JP04166.
XX PR 23-JUN-1999; 99JP-0177549.
XX PA (SHIO) SHIONOGI & CO LTD.
XX PI Yanagita T;
XX DR WPI: 2001-080754/09.
XX DR N-PSDB; AAF29139.
XX CC Composition for promoting passive elongation of vesicle smooth muscle comprises adrenomedullin

XX PS Disclosure; Page 31-33; 42pp; Japanese.

XX CC This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedullin, and has uterine contraction activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedullin protein, which is used in the composition of the invention.

XX SQ Sequence 188 AA;

Query Match 97.3%; Score 213; DB 22; Length 188;
Best Local Similarity 97.5%; Pred. No. 8.2e-23;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 40
Db 107 SFGCRFGTCTVQKLAHQIYQFTDKDNVAPRSKISPGY 146

RESULT 14
AAB60345
ID AAB60345 standard; Protein; 188 AA.
XX AC AAB60345;
XX DT 06-APR-2001 (first entry)
XX DE Porcine adrenomedullin precursor.
XX KW Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;

KW uterine contraction inhibitor; premature birth; miscarriage; abortion;
KW dysmenorrhea; obstetric; gynaecological.
XX Sus scrofa.
OS
PN WO200078339-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-JP04167.
XX
XX 23-JUN-1999; 99JP-0177548.
PR 21-MAR-2000; 2000JP-0079171.
XX
XX (SHIO) SHIONOGI & CO LTD.
PA
XX Yanagita T;
XX WPI; 2001-080755/09.
DR N-PSDB; AAF27229.
XX
XX Composition for inhibiting automatic uterine contraction or contraction
PT caused by bradykinin comprises adrenomedullin -
XX
XX Disclosure; Page 43-44; 54pp; Japanese.
XX The invention relates to a composition containing adrenomedullin for
CC inhibiting automatic uterine contraction or contraction caused by
CC bradykinin. The invention also relates to the use of adrenomedullin in
CC the preparation of a drug for preventing premature birth or miscarriage.
CC The composition of the invention can be used for preventing premature
CC birth, preventing miscarriage, stopping delivery before caesarean
CC section or for treating dysmenorrhoea. The present sequence
CC represents porcine adrenomedullin precursor.
XX
XX Sequence 188 AA;
SQ
Query Match 97.3%; Score 213; DB 22; Length 188;
Best Local Similarity 97.5%; Pred. No. 8.2e-23;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 40
DB 107 SFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 146
RESULT 15
AAB91768
ID AAB91768 standard; Peptide; 40 AA.
XX
AC AAB91768;
XX
DT 22-JUN-2001 (first entry)
XX
DE Adrenomedullin peptide (AM) SEQ ID NO:944.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX

PA (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 502; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 40 AA;
SQ
Query Match 89.5%; Score 196; DB 22; Length 40;
Best Local Similarity 87.5%; Pred. No. 4e-21;
Matches 35; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 SFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 40
DB 1 SFGCRFGTCTVOKLAHQIYQFTDKDKDNVAPRSKISPGQY 40
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